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(54) Title: NUCLEIC ACIDS AND PROTEINS FROM GROUP B STREPTOCOCCUS

(57) Abstract: Novel protein antigens from Group B Streptococcus are described, together with the nucleic acid sequences encoding them. The use of vaccines and screening methods is also described.

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Proteins

The present invention relates to proteins derived from *Streptococcus agalactiae*, nucleic acid molecules encoding such proteins, and the use of the proteins as
5 antigens and/or immunogens and in detection/diagnosis. It also relates to a method for the rapid screening of bacterial genomes to isolate and characterise bacterial cell envelope associated or secreted proteins.

The Group B Streptococcus (GBS) (*Streptococcus agalactiae*) is an encapsulated
10 bacterium which emerged in the 1970s as a major pathogen of humans causing sepsis and meningitis in neonates as well as adults. The incidence of early onset neonatal infection during the first 5 days of life varies from 0.7 to 3.7 per 1000 live births and causes mortality in about 20% of cases. Between 25-50% of neonates surviving
15 early onset infections frequently suffer neurological sequelae. Late onset neonatal infections occur from 6 days to three months of age at a rate of about 0.5 - 1.0 per 1000 live births.

There is an established association between the colonisation of the maternal genital tract by GBS at the time of birth and the risk of neonatal sepsis. In humans it has
20 been established that the rectum may act as a reservoir for GBS. Susceptibility in the neonate is correlated with the a low concentration or absence of IgG antibodies to the capsular polysaccharides found on GBS causing human disease. In the USA strains isolated from clinical cases usually belong to capsular serotypes Ia, Ib, II, III although serotype V may be of increasing significance. Type VIII GBS is the major
25 cause of neonatal sepsis in Japan.

A possible means of prevention involves intra or postpartum administration of antibiotics to the mother but there are concerns that this might lead to the emergence

of resistant organisms and in some cases allergic reactions. Vaccination of the adolescent females to induce long lasting maternally derived immunity is one of the most promising approaches to prevent GBS infections in neonates. The capsular polysaccharide antigens of these organisms have attracted most attention as with regard to vaccine development. Studies in healthy adult volunteers have shown that serotype Ia, II and III polysaccharides are non-toxic and immunogenic in approximately 65%, 95% and 70% of non-immune adults respectively. One of the problems with using capsule antigens as vaccines is that the response rates vary according to pre-immunisation status and the polysaccharide antigen and not all vaccinees produce adequate levels of IgG antibody as indicated in vaccination studies with GBS polysaccharides in human volunteers.

Some people do not respond despite repeated stimuli. These properties are due to the T-independent nature of polysaccharide antigens. One strategy to enhance the immunogenicity of these vaccines is to enhance the T cell dependent properties of polysaccharides by conjugating them to a protein. The use of polysaccharide conjugates looks promising but there are still unresolved questions concerning the nature of the carrier protein. A conjugate vaccine against GBS would require at least 4 different conjugates to be prepared adding to the cost of a vaccine.

Approaches to vaccination against GBS infections which rely on the use of capsular polysaccharides have the disadvantage that response rates are likely to vary considerably according to pre-immunisation status and the particular type of polysaccharide antigen used. Results of trials with conjugate vaccines in human volunteers have indicated that response rates may only be around 65% for some of the key capsule antigens (Larsson *et al.*, *Infection and Immunity* 64:3518-3523 (1996)). It is also not clear whether all individuals responding to the vaccine would have adequate levels of polysaccharide specific IgG which can cross the placenta and

afford immunity to neonates. By conjugating a protein carrier to the polysaccharide antigen it may be possible to convert them to T-cell dependent antigens and enhance their immunogenicity.

- 5 Preliminary studies with GBS type III polysaccharide-tetanus toxoid conjugate have been encouraging (Baker *et al.*, *Reviews of Infectious Diseases* 7:458-467 (1985), Baker *et al.*, *The New England Journal of Medicine* 319:1180-1185 (1988), Paoletti *et al.*, *Infection and Immunity* 64:677-679 (1996), Paoletti *et al.*, *Infection and Immunity* 62:3236-3243 (1994)) but in developed countries the use of tetanus may be
10 disadvantageous since most adults will have been immunised against tetanus within the past five years. Additional boosters with tetanus toxoid may cause adverse reactions (Boyer., *Current Opinions in Pediatrics* 7:13-18 (1995)). The polysaccharide conjugate vaccines have the disadvantage of being costly to produce and manufacture in comparison with many other kinds of vaccines. There is also the
15 possible risk of problems caused by the cross reactivity between GBS polysaccharides and sialic acid-containing human glycoproteins.

- Recent evidence suggests that bacterial surface proteins also may be useful to confer immunity. A protein called Rib which is found on most serotype III strains but rarely
20 on serotypes Ia, Ib or II confers immunity to challenge with Rib expressing GBS in animal models (Stalhammar-Carlemalm *et al.*, *Journal of Experimental Medicine* 177:1593-1603 (1993)). Another surface protein of interest as a component of a vaccine is the alpha antigen of the C proteins which protected vaccinated mice against lethal infection with strains expressing alpha protein. The amount of this
25 antigen expressed by GBS strains varies markedly, however an alternative to polysaccharides as antigens is the use of protein antigens derived from GBS. Recent evidence suggest that the GBS surface associated proteins Rib and alpha C protein may be used to confer immunity to GBS infections in experimental model systems

(Stalhammar-Carlén *et al.*, (1993) [*supra*], Larsson *et al.*, (1996) [*supra*]). However these two proteins are not conserved in all serotypes of GBS which cause disease in humans. Assuming that these antigens would be immunogenic and elicit protective level responses in humans they would not confer protection against all infections caused by GBS as 10% of infectious Group B streptococci do not express Rib or C protein alpha.

This invention seeks to overcome the problem of vaccination against GBS by using a novel screening method specifically designed to identify those Group B Streptococcus genes encoding bacterial cell surface associated or secreted proteins. The proteins expressed by these genes may be immunogenic, and therefore may be useful in the prevention and treatment of Group B Streptococcus infection. For the purposes of this application, the term immunogenic means that these proteins will elicit a protective immune response within a subject. Using this novel screening method a number of genes encoding novel Group B Streptococcus proteins have been identified.

Thus in a first aspect, the present invention provides a Group B Streptococcus protein, polypeptide or peptide having a sequence selected from those shown in figure 1, or fragments or derivatives thereof.

It will be apparent to the skilled person that proteins and polypeptides included within this group may be cell surface receptors, adhesion molecules, transport proteins, membrane structural proteins, and/or signalling molecules.

Alterations in the amino acid sequence of a protein can occur which do not affect the function of a protein. These include amino acid deletions, insertions and substitutions and can result from alternative splicing and/or the presence of multiple translation

start sites and stop sites. Polymorphisms may arise as a result of the infidelity of the translation process. Thus changes in amino acid sequence may be tolerated which do not affect the protein's function.

5 Thus, the present invention includes derivatives or variants of the proteins, polypeptides, and peptides of the present invention which show at least 50% identity to the proteins, polypeptides and peptides described herein. Preferably the degree of sequence identity is at least 60% and preferably it is above 75%. More preferably still it is above 80%, 90% or even 95%.

10

The term identity can be used to describe the similarity between two polypeptide sequences. A software package well known in the art for carrying out this procedure is the CLUSTAL program. It compares the amino acid sequences of two polypeptides and finds the optimal alignment by inserting spaces in either sequence as appropriate. The amino acid identity or similarity (identity plus conservation of amino acid type) for an optimal alignment can also be calculated using a software package such as BLASTx. This program aligns the largest stretch of similar sequence and assigns a value to the fit. For any one pattern comparison several regions of similarity may be found, each having a different score. One skilled in the art will appreciate that two polypeptides of different lengths may be compared over the entire length of the longer fragment. Alternatively small regions may be compared. Normally sequences of the same length are compared for a useful comparison to be made.

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Manipulation of the DNA encoding the protein is a particularly powerful technique for both modifying proteins and for generating large quantities of protein for purification purposes. This may involve the use of PCR techniques to amplify a desired nucleic acid sequence. Thus the sequence data provided herein can be used to

design primers for use in PCR so that a desired sequence can be targeted and then amplified to a high degree.

Typically primers will be at least five nucleotides long and will generally be at least ten
5 nucleotides long (e.g. fifteen to twenty-five nucleotides long). In some cases primers
of at least thirty or at least thirty-five nucleotides in length may be used.

As a further alternative chemical synthesis may be used. This may be automated.
Relatively short sequences may be chemically synthesised and ligated together to
10 provide a longer sequence.

Thus in a further aspect, the present invention provides, a nucleic acid molecule
comprising or consisting of a sequence which is:

- 15 (i) any of the DNA sequences set out in figure 1 herein or their RNA
equivalents;
- (ii) a sequence which is complementary to any of the sequences of (i);
- (iii) a sequence which codes for the same protein or polypeptide, as those
sequences of (i) or (ii);
- (iv) a sequence which shows substantial identity with any of those of (i),
20 (ii) and (iii); or
- (v) a sequence which codes for a derivative or fragment of a nucleic acid
molecule shown in figure 1.

The term identity can also be used to describe the similarity between two individual
DNA sequences. The 'bestfit' program (Smith and Waterman, *Advances in applied*
25 *Mathematics*, 482-489 (1981)) is one example of a type of computer software used to
find the best segment of similarity between two nucleic acid sequences, whilst the
GAP program enables sequences to be aligned along their whole length and finds the
optimal alignment by inserting spaces in either sequence as appropriate.

The present invention includes nucleic acid sequences which show at least 50% identity to the nucleic acid sequences described herein. Preferably the degree of sequence identity is at least 60% and preferably it is above 75%. More preferably still it is above 80%, 90% or even 95%.

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The term 'RNA equivalent' when used above indicates that a given RNA molecule has a sequence which is complementary to that of a given DNA molecule, allowing for the fact that in RNA 'U' replaces 'T' in the genetic code. The nucleic acid molecule may be in isolated, recombinant or chemically synthetic form.

10

DNA constructs can readily be generated using methods well known in the art. These techniques are disclosed, for example in J. Sambrook *et al*, *Molecular Cloning 2nd Edition*, Cold Spring Harbour Laboratory Press (1989). Modifications of DNA constructs and the proteins expressed such as the addition of promoters, enhancers, signal sequences, leader sequences, translation start and stop signals and DNA stability controlling regions, or the addition of fusion partners may then be facilitated.

15

Normally the DNA construct will be inserted into a vector which may be any suitable vector, including plasmid, virus, bacteriophage, transposon, minichromosome, liposome or mechanical carrier. The expression vectors of the invention are DNA constructs suitable for expressing DNA which encodes the desired protein product which may include: (a) a regulatory element (e.g. a promoter, operator, activator, repressor and/or enhancer), (b) a structural or coding sequence which is transcribed into mRNA and (c) appropriate transcription, translation, initiation and termination sequences. The vector may further comprise a selectable marker, for example antibiotic resistance, which facilitates the selection and/or identification of cells containing the vector.

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Expression of the protein is achieved by the transformation or transfection of the vector into a host cell which may be of eukaryotic or prokaryotic origin. For the production of recombinant protein, expression may be inducible expression or
5 expression only in certain types of cells or both inducible and cell-specific. Particularly preferred among inducible vectors are vectors that can be induced for expression by environmental factors that are easy to manipulate, such as temperature and nutrient additives. A variety of suitable vectors, including constitutive and inducible expression vectors for use in prokaryotic and eukaryotic
10 hosts, are well known and employed routinely by those skilled in the art.

A great variety of expression vectors can be used to express the Group B Streptococcus protein(s) of the invention. Such vectors include, among others, chromosomal, episomal and virus-derived vectors, for example, vectors derived
15 from bacterial plasmids, from bacteriophage, from transposons, from yeast elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids, all may be used in accordance with the invention. Generally, any
20 vector suitable to maintain, propagate or express nucleic acid to express a polypeptide in a host may be used for expression in this regard. Such vectors thus form yet a further aspect of the invention.

The appropriate DNA sequence may be inserted into the vector by any of a variety
25 of well-known and routine techniques.

The nucleic acid sequence in the expression vector is operatively linked to appropriate expression control sequence(s) including, for instance, a promoter to

direct mRNA transcription. Representatives of such promoters include, but are not limited to, the phage lambda PL promoter, the T3 and T7 promoters, the *E.coli* lac, trp, tac, and λ P_L promoters, the microbial eukaryote GAL, glucoamylase and cellobiohydrolase promoters and the mammalian metallothionein (mouse) and heat-shock (human) promoters.

In general, expression vectors will contain sites for transcription initiation and termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of mature transcripts expressed by the constructs will generally include a translation initiating AUG at the beginning and a termination codon appropriately positioned at the end of the polypeptide to be translated.

Representative examples of appropriate hosts for recombinant expression of the Group B Streptococcus protein(s) of the invention include bacterial cells, such as *streptococci*, *staphylococci*, *E.coli*, *streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa and Bowes melanoma cells; and plant cells. Such host cells form yet a further aspect of the present invention.

Microbial cells employed in the expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agent, such methods which are known to those skilled in the art.

The polypeptide can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose,

chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Well known techniques for refolding protein may be employed to regenerate active conformation when the polypeptide is denatured during isolation and or purification.

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The Group B Streptococcus proteins described herein can additionally be used as target antigens to raise antibodies, or to generate affibodies. These can be used to detect Group B Streptococcus.

10 Thus in a further aspect the present invention provides, an antibody, affibody, or a derivative thereof which binds to any one or more of the proteins, polypeptides, peptides, fragments or derivatives thereof, as described herein.

Antibodies within the scope of the present invention may be monoclonal or polyclonal.

15 Polyclonal antibodies can be raised by stimulating their production in a suitable animal host (e.g. a mouse, rat, guinea pig, rabbit, sheep, goat or monkey) when a protein as described herein, or a homologue, derivative or fragment thereof, is injected into the animal. If desired, an adjuvant may be administered together with the protein. Well-known adjuvants include Freund's adjuvant (complete and incomplete) and aluminium
20 hydroxide. The antibodies can then be purified by virtue of their binding to a protein as described herein and by many other means well-known to those skilled in the art.

Monoclonal antibodies can be produced from hybridomas. These can be formed by fusing myeloma cells and spleen cells which produce the desired antibody in order to
25 form an immortal cell line. Thus the well-known Kohler & Milstein technique (*Nature* 256 (1975)) or subsequent variations upon this technique can be used.

Techniques for producing monoclonal and polyclonal antibodies that bind to a particular polypeptide/protein are now well developed in the art. They are discussed in standard immunology textbooks, for example in Roitt *et al*, *Immunology* second edition (1989), Churchill Livingstone, London.

5

In addition to whole antibodies, the present invention includes derivatives thereof which are capable of binding to proteins etc as described herein. Thus the present invention includes antibody fragments and synthetic constructs. Examples of antibody fragments and synthetic constructs are given by Dougall *et al*., *Tibtech* 12 372-379 (September 1994).

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Antibody fragments include, for example, Fab, F(ab')₂ and Fv fragments. Fv fragments can be modified to produce a synthetic construct known as a single chain Fv (scFv) molecule. This includes a peptide linker covalently joining V_H and V_L regions, which contributes to the stability of the molecule. Other synthetic constructs that can be used include CDR peptides. These are synthetic peptides comprising antigen-binding determinants. Peptide mimetics may also be used. These molecules are usually conformationally restricted organic rings that mimic the structure of a CDR loop and that include antigen-interactive side chains.

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Synthetic constructs include chimaeric molecules. Thus, for example, humanised (or primatised) antibodies or derivatives thereof are within the scope of the present invention. An example of a humanised antibody is an antibody having human framework regions, but rodent hypervariable regions. Ways of producing chimaeric antibodies are discussed for example by Morrison *et al* in *PNAS*, 81, 6851-6855 (1984) and by Takeda *et al* in *Nature*. 314, 452-454 (1985).

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Synthetic constructs also include molecules comprising an additional moiety that provides the molecule with some desirable property in addition to antigen binding. For example the moiety may be a label (e.g. a fluorescent or radioactive label). Alternatively, it may be a pharmaceutically active agent.

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Affibodies are proteins which are found to bind to target proteins with a low dissociation constant. They are selected from phage display libraries expressing a segment of the target protein of interest (Nord K, Gunneriusson E, Ringdahl J, Stahl S, Uhlen M, Nygren PA, Department of Biochemistry and Biotechnology, Royal Institute of Technology (KTH), Stockholm, Sweden).

10

In a further aspect the invention provides an immunogenic composition comprising one or more proteins, polypeptides, peptides, fragments or derivatives thereof, or nucleotide sequences described herein. The immunogenic composition may include nucleic acid sequences ID-65 and/or ID-66 as described herein. Alternatively, the immunogenic composition may comprise proteins/polypeptides including ID-65, ID-83, ID-89, ID-93 and/or ID-96 as described herein, or fragments or derivatives thereof. A composition of this sort may be useful in the treatment or prevention of Group B Streptococcus infection in subject. In a preferred aspect of the invention the immunogenic composition is a vaccine.

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In other aspects the invention provides:

- i) Use of an immunogenic composition as described herein in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. Preferably the medicament is a vaccine.

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- ii) A method of detection of Group B Streptococcus which comprises the step of bringing into contact a sample to be tested with at least one antibody, affibody, or a derivative thereof, as described herein.
- 5 iii) A method of detection of Group B Streptococcus which comprises the step of bringing into contact a sample to be tested with at least one protein, polypeptide, peptide, fragments or derivatives as described herein.
- 10 iv) A method of detection of Group B Streptococcus which comprises the step of bringing into contact a sample to be tested with at least one nucleic acid molecule as described herein.
- 15 v) A kit for the detection of Group B Streptococcus comprising at least one antibody, affibody, or derivatives thereof, described herein.
- 15 vi) A kit for the detection of Group B Streptococcus comprising at least one Group B Streptococcus protein, polypeptide, peptide, fragment or derivative thereof, as described herein.
- 20 vii) A kit for the detection of Group B Streptococcus comprising at least one nucleic acid of the invention.

As described previously, the novel proteins described herein are identified and isolated using a screening method which specifically identifies those Group B
25 Streptococcus genes encoding bacterial cell envelope associated or secreted proteins.

Given that the inventors have identified a group of important proteins, such proteins are potential targets for anti-microbial therapy. It is necessary, however, to

determine whether each individual protein is essential for the organism's viability. Thus, the present invention also provides a method of determining whether a protein or polypeptide as described herein represents a potential anti-microbial target which comprises inactivating said protein and determining whether Group B Streptococcus is still viable.

A suitable method for inactivating the protein is to effect selected gene knockouts, ie prevent expression of the protein and determine whether this results in a lethal change. Suitable methods for carrying out such gene knockouts are described in Li *et al* , *P.N.A.S.*, **94**:13251-13256 (1997) and Kolkman *et al.*, *Journal of Biological Chemistry* **272**: 19502-19508 (1997); Kolkman *et al.*, *Journal of Bacteriology* **178**: 3736-3741 (1996).

In a final aspect the present invention provides the use of an agent capable of antagonising, inhibiting or otherwise interfering with the function or expression of a protein or polypeptide of the invention in the manufacture of a medicament for use in the treatment or prophylaxis of Group B Streptococcus infection.

The invention will now be described by means of the following examples which should not in any way be construed as limiting. The examples refer to the figures in which:

Fig 1: (A) Shows a number of full length nucleotide sequences encoding antigenic Group B Streptococcus proteins and the corresponding amino acid sequences.

Fig 2: Shows the results of vaccine trials using the proteins ID-65 and ID-66;

Fig 3: Shows a number of oligonucleotide primers used in the screening process

nucS1 primer designed to amplify a mature form of the *nuc A* gene

nucS2- primer designed to amplify a mature form of the *nuc A* gene.

5 **nucS3** primer designed to amplify a mature form of the *nuc A* gene

nucR primer designed to amplify a mature form of the *nuc A* gene

nucseq primer designed to sequence DNA cloned into the pTREP-Nuc vector

pTREPF nucleic acid sequence containing recognition site for *ECORV*. Used for cloning fragments into pTREX7.

10 **pTREPR** nucleic acid sequence containing recognition site for *BAMH1*. Used for cloning fragments into pTREX7.

PUCF forward sequencing primer, enables direct sequencing of cloned DNA fragments.

15 **VR** example of gene specific primer used to obtain further antigen DNA sequence by the method of DNA walking.

V1 example of gene specific primer used to obtain further antigen DNA sequence by the method of DNA walking.

V2 example of gene specific primer used to obtain further antigen DNA sequence by the method of DNA walking.

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Fig 4: (i) Schematic presentation of the nucleotide sequence of the unique gene cloning site immediately upstream of the mature *nuc* gene in pTREP1-*nuc1*, pTREP1-*nuc2* and pTREP1-*nuc3*. Each of the pTREP-*nuc* vectors contain an *EcoRV* (a *SmaI* site in pTREP1-*nuc2*) cleavage site which allows cloning of genomic DNA fragments in 3 different frames with respect to the mature *nuc* gene.

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(ii) A physical and genetic summary map of the pTREP1-*nuc* vectors. The expression cassette incorporating *nuc*, the macrolides, lincosamides and

streptogramin B (MLS) resistance determinant, and the replicon (rep) *Ori-pAM* β 1 are depicted (not drawn to scale).

(iii) Schematic presentation of the expression cassette showing the various sequence elements involved in gene expression and location of unique restriction endonuclease sites (not drawn to scale).

Fig 5: SDS-PAGE analysis of a purified preparation of the His-tagged ID-65 and ID-83 protein antigens (predicted molecular weights of 57,144 and 25,000 daltons respectively) on a 12% polyacrylamide gel. Lanes: MW, molecular weight standards; 1, His-tagged ID-65 protein; 2, His-tagged ID-83 protein

Fig 6: SDS PAGE analysis of a purified preparation of the His-tagged ID-93 protein antigen (predicted molecular weight = 28,000 daltons) on a 12% polyacrylamide gel.

Lanes: MW, molecular weight standards; 1, His-tagged ID-93 protein.

Fig 7: SDS PAGE analysis of a purified preparation of the His-tagged ID-89 and ID-96 protein antigens (predicted molecular weights of 35,000 and 31,000 daltons respectively) on a 12% polyacrylamide gel.

Lanes: MW, molecular weight standards; 1, His-tagged ID-89 protein; 2, His-tagged ID-96 protein.

Fig 8: IgG Titres against the ID-65 and ID-83 proteins

1 = ID-65 + Alum Group - Bleed at 5 weeks

2 = PBS + Alum Control Group - Bleed at 5 weeks

(For groups 1 and 2, ELISAs were performed on purified ID-65 protein)

3 = ID-83 + Alum Group - Bleed at 5 weeks

17.

4 = PBS+ Alum Control Group – Bleed at 5 weeks

(For groups 3 and 4, ELISAs were performed on purified ID-83 protein)

Fig 9: Shows the results of vaccine trials using the protein ID-93.

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Fig 10: IgG titres against the ID-93 protein.

1 = ID-93+ Alum Group – Bleed at 3 weeks

2 = ID-93+ Alum Group – Bleed at 6 weeks

3 = PBS+ Alum Control Group – Bleed at 3 weeks

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4 = PBS+ Alum Control Group – Bleed at 6 weeks

Fig 11: IgG titres against the ID-89 and ID-96 proteins

1 = ID-89+ TitreMax Gold Group – Bleed at 3 weeks

2 = ID-89+ TitreMax Gold – Bleed at 6 weeks

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3 = PBS+ TitreMax Gold Control Group – Bleed at 3 weeks

4 = PBS+ TitreMax Gold Control Group – Bleed at 6 weeks

5 = ID-96+ TitreMax Gold Group – Bleed at 3 weeks

6 = ID-96+ TitreMax Gold Group – Bleed at 6 weeks

7 = PBS+ TitreMax Gold Control Group – Bleed at 3 weeks

20

8 = PBS+ TitreMax Gold Control Group – Bleed at 6 weeks

For Groups 1-4, ELISAs were performed on purified ID-89 protein.

For Groups 5-6, ELISAs were performed on purified ID-96 protein.

Fig 12: Southern blot analysis of genomic DNA. Genomic DNA from each of the strains listed in Table 7 was digested completely with *Hin* DIII (NEB) and electrophoresed at 40 Volts for 6 hours in 0.8% agarose, transferred onto Hybond N⁺ (Amersham) membrane by Southern blot and hybridised with the

25

digoxigenin-labelled *rib* gene probe. Specifically bound DNA probe was identified using the DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

Fig 13: Southern blot analysis of genomic DNA. Genomic DNA from each of the strains listed in Table 6 was digested completely with *Hin* DIII (NEB) and electrophoresed at 40 Volts for 6 hours in 0.8% agarose, transferred onto Hybond N⁺ (Amersham) membrane by Southern blot and hybridised with the digoxigenin-labelled ID-65 gene probe. Specifically bound DNA probe was identified using the DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

Fig 14: Southern blot analysis of genomic DNA. Genomic DNA from each of the strains listed in Table 6 was digested completely with *Hin* DIII (NEB) and electrophoresed at 40 Volts for 6 hours in 0.8% agarose, transferred onto Hybond N⁺ (Amersham) membrane by Southern blot and hybridised with the digoxigenin-labelled ID-89 gene probe. Specifically bound DNA probe was identified using the DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

Fig 15: Southern blot analysis of genomic DNA. Genomic DNA from each of the strains listed in Table 6 was digested completely with *Hin* DIII (NEB) and electrophoresed at 40 Volts for 6 hours in 0.8% agarose, transferred onto Hybond N⁺ (Amersham) membrane by Southern blot and hybridised with the digoxigenin-labelled ID-93 gene probe. Specifically bound DNA probe was identified using the DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

Fig 16: Southern blot analysis of genomic DNA. Genomic DNA from each of the strains listed in Table 6 was digested completely with *Eco* RI (NEB) and electrophoresed at 40 Volts for 6 hours in 0.8% agarose, transferred onto Hybond N⁺ (Amersham) membrane by Southern blot and hybridised with the

digoxigenin-labelled ID-96 gene probe. Specifically bound DNA probe was identified using the DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

5

Example 1

Gene/partial gene sequences putatively encoding exported proteins in *S. agalactiae* have been identified, unless stated otherwise, using the nuclease screening system described herein *vis*, the LEEP (Lactococcus Expression of Exported Proteins) system. These have been further analysed to remove artefacts. The nucleotide sequences of genes identified using the screening system have been characterised using a number of parameters described below.

15 1. All putative surface proteins are analysed for leader/signal peptide sequences. Bacterial signal peptide sequences share a common design. They are characterised by a short positively charged N-terminus (N region) immediately preceding a stretch of hydrophobic residues (central portion-h region) followed by a more polar C-terminal portion which contains the cleavage site (c-region). Computer software is used to perform hydropathy profiling of putative proteins (Marcks, *Nuc. Acid. Res.*, 16:1829-1836 (1988)) which is used to identify the distinctive hydrophobic portion (h-region) typical of leader peptide sequences. In addition, the presence/absence of a potential ribosomal binding site (Shine-Dalgarno sequence required for translation) is also noted.

25 2. All putative surface protein sequences are used to search the OWL sequence database which includes a translation of the GENBANK and SWISSPROT database.. This allows identification of similar sequences which may have been previously characterised not only at the sequence level but at a functional level. It

may also provide information indicating that these proteins are indeed surface related and not artefacts.

3. Putative *S. agalactiae* surface proteins are also assessed for their novelty. Some of the identified proteins may or may not possess a typical leader peptide sequence and may not show homology with any DNA/protein sequences in the database. Indeed these proteins may indicate the primary advantage of our screening method, i.e. isolating atypical surface-related proteins, which would have been missed in all previously described screening protocols.

10 The construction of three reporter vectors and their use in *L. lactis* to identify and isolate genomic DNA fragments from pathogenic bacteria encoding secreted or surface associated proteins is now described.

Construction of the pTREP1-*nuc* series of reporter vectors

15 (a) Construction of expression plasmid pTREP1

The pTREP1 plasmid is a high-copy number (40-80 per cell) theta-replicating gram positive plasmid, which is a derivative of the pTREX plasmid which is itself a derivative of the previously published pIL253 plasmid. pIL253 incorporates the broad Gram-positive host range replicon of pAM β 1 (Simon and Chopin, *Biochemie* 20 70: 559-566 (1988)) *L. lactis* sex-factor. pIL253 also lacks the *tra* function which is necessary for transfer or efficient mobilisation by conjugative parent plasmids exemplified by pIL501. The Enterococcal pAM β 1 replicon has previously been transferred to various species including *Streptococcus*, *Lactobacillus* and *Bacillus* 25 species as well as *Clostridium acetobutylicum*, (LeBlanc *et al.*, *Proceedings of the National Academy of Science USA* 75:3484-3487 (1978)) indicating the potential broad host range utility. The pTREP1 plasmid represents a constitutive transcription vector.

The pTREX vector was constructed as follows. An artificial DNA fragment containing a putative RNA stabilising sequence, a translation initiation region (TIR), a multiple cloning site for insertion of the target genes and a transcription terminator was created by annealing 2 complementary oligonucleotides and extending with Tfl DNA polymerase. The sense and anti-sense oligonucleotides contained the recognition sites for NheI and BamHI at their 5' ends respectively to facilitate cloning. This fragment was cloned between the XbaI and BamHI sites in pUC19NT7, a derivative of pUC19 which contains the T7 expression cassette from pLET1 (Wells *et al.*, *J. Appl. Bacteriol.* 74:629-636 (1993)) cloned between the EcoRI and HindIII sites. The resulting construct was designated pUCLEX. The complete expression cassette of pUCLEX was then removed by cutting with HindIII and blunting followed by cutting with EcoRI before cloning into EcoRI and SacI (blunted) sites of pIL253 to generate the vector pTREX (Wells and Schofield, *In* Current advances in metabolism, genetics and applications-NATO ASI Series. H 98:37-62. (1996)). The putative RNA stabilising sequence and TIR are derived from the *Escherichia coli* T7 bacteriophage sequence and modified at one nucleotide position to enhance the complementarity of the Shine Dalgarno (SD) motif to the ribosomal 16s RNA of *Lactococcus lactis* (Schofield *et al.* pers. coms. University of Cambridge Dept. Pathology.).

A *Lactococcus lactis* MG1363 chromosomal DNA fragment exhibiting promoter activity which was subsequently designated P7 was cloned between the EcoRI and BglII sites present in the expression cassette, creating pTREX7. This active promoter region had been previously isolated using the promoter probe vector pSB292 (Waterfield *et al.*, *Gene* 165:9-15 (1995)). The promoter fragment was amplified by PCR using the Vent DNA polymerase according to the manufacturer.

The pTREP1 vector was then constructed as follows. An artificial DNA fragment which included a transcription terminator, the forward pUC sequencing primer, a promoter multiple cloning site region and a universal translation stop sequence was created by annealing two overlapping partially complementary synthetic oligonucleotides together and extending with sequenase according to manufacturers instructions. The sense and anti-sense (pTREPF and pTREP R) oligonucleotides contained the recognition sites for EcoRV and BamHI at their 5' ends respectively to facilitate cloning into pTREX7. The transcription terminator was that of the *Bacillus penicillinase* gene, which has been shown to be effective in *Lactococcus* (Jos *et al.*, *Applied and Environmental Microbiology* 50:540-542 (1985)). This was considered necessary as expression of target genes in the pTREX vectors was observed to be leaky and is thought to be the result of cryptic promoter activity in the origin region (Schofield *et al.* pers. coms. University of Cambridge Dept. Pathology.). The forward pUC primer sequencing was included to enable direct sequencing of cloned DNA fragments. The translation stop sequence which encodes a stop codon in 3 different frames was included to prevent translational fusions between vector genes and cloned DNA fragments. The pTREX7 vector was first digested with EcoRI and blunted using the 5' - 3' polymerase activity of T4 DNA polymerase (NEB) according to manufacturer's instructions. The EcoRI digested and blunt ended pTREX7 vector was then digested with Bgl II thus removing the P7 promoter. The artificial DNA fragment derived from the annealed synthetic oligonucleotides was then digested with EcoRV and Bam HI and cloned into the EcoRI(blunted)-Bgl II digested pTREX7 vector to generate pTREP. A *Lactococcus lactis* MG1363 chromosomal promoter designated P1 was then cloned between the EcoRI and BglII sites present in the pTREP expression cassette forming pTREP1. This promoter was also isolated using the promoter probe vector pSB292 and characterised by Waterfield *et al.*, (1995) [*supra*]. The P1 promoter fragment was originally amplified by PCR using vent DNA polymerase according to manufacturers

instructions and cloned into the pTREX as an EcoRI-BglII DNA fragment. The EcoRI-BglII P1 promoter containing fragment was removed from pTREX1 by restriction enzyme digestion and used for cloning into pTREP (Schofield *et al.* pers. coms. University of Cambridge, Dept. Pathology.).

5

(b) PCR amplification of the *S. aureus* nuc gene.

The nucleotide sequence of the *S. aureus* nuc gene (EMBL database accession number V01281) was used to design synthetic oligonucleotide primers for PCR
10 amplification. The primers were designed to amplify the mature form of the nuc gene designated nucA which is generated by proteolytic cleavage of the N-terminal 19 to 21 amino acids of the secreted propeptide designated Snase B (Shortle, 1983 [supra]). Three sense primers (nucS1, nucS2 and nucS3, shown in figure 3) were designed, each one having a blunt-ended restriction endonuclease cleavage site for
15 EcoRV or SmaI in a different reading frame with respect to the nuc gene. Additionally BglII and BamHI were incorporated at the 5' ends of the sense and anti-sense primers respectively to facilitate cloning into BamHI and BglII cut pTREP1. The sequences of all the primers are given in figure 3. Three nuc gene DNA fragments encoding the mature form of the nuclease gene (NucA) were amplified by
20 PCR using each of the sense primers combined with the anti-sense primer. The nuc gene fragments were amplified by PCR using *S. aureus* genomic DNA template, Vent DNA Polymerase (NEB) and the conditions recommended by the manufacturer. An initial denaturation step at 93°C for 2 min was followed by 30 cycles of denaturation at 93°C for 45 sec, annealing at 50°C for 45 seconds, and extension at
25 73°C for 1 minute and then a final 5 min extension step at 73°C. The PCR amplified products were purified using a Wizard clean up column (Promega) to remove unincorporated nucleotides and primers.

(c) Construction of the pTREP1-nuc vectors

The purified *nuc* gene fragments described in section b were digested with Bgl II and BamHI using standard conditions and ligated to BamHI and BglII cut and dephosphorylated pTREP1 to generate the pTREP1-*nuc*1, pTREP1-*nuc*2 and pTREP1-*nuc*3 series of reporter vectors. These vectors are described in figure 4. General molecular biology techniques were carried out using the reagents and buffers supplied by the manufacturer or using standard techniques (Sambrook and Maniatis, Molecular cloning: A laboratory manual. Cold Spring Harbor Laboratory Press: Cold Spring Harbour (1989)). In each of the pTREP1-*nuc* vectors the expression cassette comprises a transcription terminator, lactococcal promoter P1, unique cloning sites (Bgl II, EcoRV or SmaI) followed by the mature form of the *nuc* gene and a second transcription terminator. Note that the sequences required for translation and secretion of the *nuc* gene were deliberately excluded in this construction. Such elements can only be provided by appropriately digested foreign DNA fragments (representing the target bacterium) which can be cloned into the unique restriction sites present immediately upstream of the *nuc* gene.

(d) Screening for secreted proteins in Group B Streptococcus.

Genomic DNA isolated from Group B Streptococcus (*S. agalactiae*) was digested with the restriction enzyme Tru9I. This enzyme which recognises the sequence 5'-TTAA -3' was used because it cuts A/T rich genomes efficiently and can generate random genomic DNA fragments within the preferred size range (usually averaging 0.5 - 1.0 kb). This size range was preferred because there is an increased probability that the P1 promoter can be utilised to transcribe a novel gene sequence. However, the P1 promoter may not be necessary in all cases as it is possible that many Streptococcal promoters are recognised in *L. lactis*. DNA fragments of different size ranges were purified from partial Tru9I digests of *S. agalactiae* genomic DNA. As

the Tru 9I restriction enzyme generates staggered ends the DNA fragments had to be made blunt ended before ligation to the EcoRV or SmaI cut pTREP1-*nuc* vectors. This was achieved by the partial fill-in enzyme reaction using the 5'-3' polymerase activity of Klenow enzyme. Briefly Tru9I digested DNA was dissolved in a solution (usually between 10-20 μ l in total) supplemented with T4 DNA ligase buffer (New England Biolabs; NEB) (1X) and 33 μ M of each of the required dNTPs, in this case dATP and dTTP. Klenow enzyme was added (1 unit Klenow enzyme (NEB) per μ g of DNA) and the reaction incubated at 25°C for 15 minutes. The reaction was stopped by incubating the mix at 75°C for 20 minutes. EcoRV or SmaI digested pTREP-*nuc* plasmid DNA was then added (usually between 200-400 ng). The mix was then supplemented with 400 units of T4 DNA ligase (NEB) and T4 DNA ligase buffer (1X) and incubated overnight at 16°C. The ligation mix was precipitated directly in 100% Ethanol and 1/10 volume of 3M sodium acetate (pH 5.2) and used to transform *L. lactis* MG1363 (Gasson, *J. Bacteriol.* 154:1-9 (1983)). Alternatively, the gene cloning site of the pTREP-*nuc* vectors also contains a BglII site which can be used to clone for example Sau3AI digested genomic DNA fragments.

L. lactis transformant colonies were grown on brain heart infusion agar and nuclease secreting (*Nuc*⁺) clones were detected by a toluidine blue-DNA-agar overlay (0.05 M Tris pH 9.0, 10 g of agar per litre, 10 g of NaCl per liter, 0.1 mM CaCl₂, 0.03% wt/vol. salmon sperm DNA and 90 mg of Toluidine blue O dye) essentially as described by Shortle, 1983 [*supra*], and Le Loir *et al.*, 1994 [*supra*]). The plates were then incubated at 37°C for up to 2 hours. Nuclease secreting clones develop an easily identifiable pink halo. Plasmid DNA was isolated from *Nuc*⁺ recombinant *L. lactis* clones and DNA inserts were sequenced on one strand using the *NucSeq* sequencing primer described in figure 3, which sequences directly through the DNA insert.

Example 2

Preparation of a *S. agalactiae* standard inoculum

5 Strain validation

S. agalactiae serotype III (strain 97/0099) is a recent clinical isolate derived from the cerebral spinal fluid of a new born baby suffering from meningitis. This haemolytic strain of Group B Streptococcus was epidemiologically tested and validated at the Respiratory and Systemic Infection Laboratory, PHLS Central Public Health
10 Laboratory, 61 Colindale Avenue, London NW9 5HT. The strain was subcultured only twice prior to its arrival in the laboratory. Upon its arrival on an agar slope, a sweep of 4-5 colonies was immediately used to inoculate a Todd Hewitt/5% horse blood broth which was incubated overnight statically at 37°C. 0.5 ml aliquots of this overnight culture were then used to make 20% glycerol stocks of the bacterium for
15 long-term storage at -70°C. Glycerol stocks were streaked on Todd Hewitt/5% horse blood agar plates to confirm viability.

In vivo passaging of Group B Streptococcus

A frozen culture (described under strain validation) of *S. agalactiae* serotype III
20 (strain 97/0099) was streaked to single colonies on Todd-Hewitt/5% blood agar plates, which were incubated overnight at 37°C. A sweep of 4-5 colonies was used to inoculate a Todd Hewitt/5% horse blood broth, which was again incubated overnight. A 0.5 ml aliquot from this overnight culture was used to inoculate a 50 ml Todd Hewitt broth (1:100 dilution) which was incubated at 37°C. 10-fold serial
25 dilutions of the overnight culture were made (since virulence of this strain was unknown) and each was passaged intra-peritoneally (IP) in CBA/ca mice in duplicate. Viable counts were performed on the various inocula used in the passage. Groups of mice were challenged with various concentrations of the pathogen ranging from 10⁸ to 10⁴ colony forming units (cfu). Mice that developed symptoms were
30 terminally anaesthetized and cardiac punctures were performed (Only mice that had

been challenged with the highest doses, i.e. 1×10^8 cfu, developed symptoms). The retrieved unclotted blood was used to inoculate directly a 50ml serum broth (Todd Hewitt/20% inactivated foetal calf serum). The culture was constantly monitored and allowed to grow to late logarithmic phase. The presence of blood in the medium
5 interfered with OD_{600nm} readings as it was being increasingly lysed with increasing growth of the bacterium, hence the requirement to constantly monitor the culture. Upon reaching late logarithmic phase/early stationary phase, the culture was transferred to a fresh 50 ml tube in order to exclude dead bacterial cells and remaining blood cells which would have sedimented at the bottom of the tube. 0.5
10 ml aliquots were then transferred to sterile cryovials, frozen in liquid nitrogen and stored at -70°C. A viable count was carried out on a single standard inoculum aliquot in order to determine bacterial numbers. This was determined to be approximately 5×10^8 cfu per ml.

15 **Intra-peritoneal Challenge and virulence testing of Group B Streptococcus standard inoculum**

To determine if the standard inoculum was suitably virulent for use in a vaccine trial, challenges were carried out using a dose range. Frozen standard inoculum strain aliquots were allowed to thaw at room temperature. From viable count data the
20 number of cfu per ml was already known for the standard inoculum. Initially, serial dilutions of the standard inoculum were made in Todd Hewitt broth and mice were challenged intra-peritoneally with doses ranging from 1×10^8 to 1×10^4 cfu in a 500 μ l volume of Todd Hewitt broth. The survival times of mouse groups injected with different doses of the bacterium were compared. The standard inoculum was
25 determined to be suitably virulent and a dose of 1×10^6 cfu was considered close to optimal for further use in vaccine trials. Further optimisation was carried out by comparing mice challenged with doses ranging between 5×10^5 and 5×10^6 cfu. The optimal dose was estimated to be approximately 2.5×10^6 cfu. This represented

a 100% lethal dose and was repeatedly consistent with end-points as determined by survival times being clustered within a narrow time-range. Throughout all these experiments, challenged mice were constantly monitored to clarify symptoms, stages of symptom development as well as calculating survival times.

5

Screening Group B Streptococcal LEEP derived genes in DNA vaccination experiments.

pcDNA3.1+ as a DNA vaccine vector

10 The commercially available pcDNA3.1+ plasmid (Invitrogen), referred to as pcDNA3.1 henceforth, was used as a vector in all DNA immunisation experiments involving gene targets derived using the LEEP system unless stated otherwise. pcDNA 3.1 is designed for high-level stable and transient expression in mammalian cells and has been used widely and successfully as a host vector to test candidate
15 genes from a variety of pathogens in DNA vaccination experiments (Zhang *et al.*, *Infection and Immunity* 176: 1035-40 (1997); Kurar and Splitter, *Vaccine* 15: 1851-57 (1997); Anderson *et al.*, *Infection and Immunity* 64: 3168-3173 (1996)).

The vector possesses a multiple cloning site which facilitates the cloning of multiple
20 gene targets downstream of the human cytomegalovirus (CMV) immediate-early promoter/enhancer which permits efficient, high-level expression of the target gene in a wide variety of mammalian cells and cell types including both muscle and immune cells. This is important for optimal immune response as it remains unknown as to which cells types are most important in generating a protective response *in*
25 *vivo*. The plasmid also contains the ColE1 origin of replication which allows convenient high-copy number replication and growth in *E. coli* and the ampicillin resistance gene (B- lactamase) for selection in *E. coli*. In addition pcDNA 3.1

possesses a T7 promoter/priming site upstream of the MCS which allows for *in vitro* transcription of a cloned gene in the sense orientation.

Preparation of DNA vaccines

5 Oligonucleotide primers were designed for each individual gene of interest derived using the LEEP system unless stated otherwise. Each gene was examined thoroughly, and where possible, primers were designed such that they targeted that portion of the gene believed to encode only the mature portion of the protein (APPENDIX I); the intention being to express those sequences that encode only the
10 mature portion of a target gene protein to would facilitate its correct folding when expressed in mammalian cells. For example, in the majority of cases primers were designed such that putative N-terminal signal peptide sequences would not be included in the final amplification product to be cloned into the pcDNA3.1 expression vector. The signal peptide directs the polypeptide precursor to the cell
15 membrane via the protein export pathway where it is normally cleaved off by signal peptidase I (or signal peptidase II if a lipoprotein). Hence the signal peptide does not make up any part of the mature protein whether it be displayed on the bacterium's surface or secreted. Where an N-terminal leader peptide sequence was not immediately obvious, primers were designed to target the whole of the gene
20 sequence for cloning and ultimately, expression in pcDNA3.1.

All forward and reverse oligonucleotide primers incorporated appropriate restriction enzyme sites to facilitate cloning into the pcDNA3.1 MCS region. All forward
primers were also designed to include the conserved Kozak nucleotide sequence 5'-
25 gccacc-3' immediately upstream of an 'atg' translation initiation codon in frame with the target gene insert. The Kozak sequence facilitates the recognition of initiator sequences by eukaryotic ribosomes. Typically, a forward primer incorporating a BamH1 restriction enzyme site the primer would begin with the sequence 5'-

cgggatccgccaccatg-3', followed by a sequence homologous to the 5' end of that part of a gene being amplified. All reverse primers incorporated a Not I restriction enzyme site sequence 5' -ttcggccgc-3'. All gene-specific forward and reverse primers were designed with compatible melting temperatures to facilitate their amplification.

All gene targets were amplified by PCR from *S. agalactiae* genomic DNA template using Vent DNA polymerase (NEB) or rTth DNA polymerase (PE Applied Biosystems) using conditions recommended by the manufacturer. A typical amplification reaction involved an initial denaturation step at 95°C for 2 minutes followed by 35 cycles of denaturation at 95°C for 30 seconds, annealing at the appropriate melting temperature for 30 seconds, and extension at 72°C for 1 minute (1 minute per kilobase of DNA being amplified). This was followed by a final extension period at 72°C for 10 minutes. All PCR amplified products were extracted once with phenol chloroform (2:1:1) and once with chloroform (1:1) and ethanol precipitated. Specific DNA fragments were isolated from agarose gels using the QIAquick Gel Extraction Kit (Qiagen). The purified amplification gene DNA fragments were digested with the appropriate restriction enzymes and cloned into the pcDNA3.1 plasmid vector using *E. coli* as a host. Successful cloning and maintenance of genes was confirmed by restriction mapping and by DNA sequencing. Recombinant plasmid DNA was isolated on a large scale (> 1.5 mg) using Plasmid Mega Kits (Qiagen).

DNA vaccination trials

DNA vaccine trials in mice were accomplished by the administration of DNA to 6 week old CBA/ca mice (Harlan, UK). Mice to be vaccinated were divided into groups of six and each group was immunised with recombinant pcDNA3.1 plasmid DNA containing a specific target-gene sequence derived using the LEEP system unless stated otherwise. A total of 100 µg of DNA in Dulbecco's PBS (Sigma) was

injected intramuscularly into the tibialis anterior muscle of both hind legs. Four weeks later this procedure was repeated using the same amount of DNA. For comparison, control mice groups were included in all vaccine trials. These control groups were either not DNA-vaccinated or were immunised with non-recombinant pcDNA3.1 plasmid DNA only, using the same time course described above. Four weeks after the second immunisation, all mice groups were challenged intra-peritoneally with a lethal dose of *S. agalactiae* serotype III (strain 97/0099). The actual number of bacteria administered was determined by plating serial dilutions of the inoculum on Todd-Hewitt/5% blood agar plates. All mice were killed 3 or 4 days after infection. During the infection process, challenged mice were monitored for the development of symptoms associated with the onset of *S. agalactiae* induced-disease. Typical symptoms in an appropriate order included piloerection, an increasingly hunched posture, discharge from eyes, increased lethargy and reluctance to move which was often the result of apparent paralysis in the lower body/hind leg region. The latter symptoms usually coincided with the development of a moribund state at which stage the mice were culled to prevent further suffering. These mice were deemed to be very close to death, and the time of culling was used to determine a survival time for statistical analysis. Where mice were found dead, a survival time was calculated by averaging the time when a particular mouse was last observed alive and the time when found dead, in order to determine a more accurate time of death. The results of this trial are shown in Table 1 and presented graphically in Figure 2.

Interpretation of Results

A positive result was taken as any DNA sequence that was cloned and used in challenge experiments as described above and gave protection against that challenge. DNA sequences were determined to be protective;

-if that DNA sequence gave statistically significant protection to mice as compared to control mice (to a 95% confidence level ($p > 0.05$) as determined using the Mann-Whitney U test .

-if that DNA sequence was marginal or non-significant using Mann-Whitney but

- 5 showed some protective features. For example, one or more outlying mice may survive for significantly longer time periods when compared with control mice. Alternatively, the time to first death may also be prolonged when compared to counterpart mice in control groups. It is acceptable to allow marginal or non-significant results to be considered as potential positives when it is possible that the
- 10 clarity of some results may be affected by problems associated with the administration of the DNA vaccine. Indeed, much varied survival times may reflect different levels of immune response between different members of a given group.

Table 1

15 **LEEP DNA immunisation and GBS challenge Experiment**

Statistical analysis of survival times

	Mean Survival Times (hours)		
	UnVacc	3-60(ID-65)	3-5(ID-66)
1	27.583	54.416	42.916
2	27.583	31.000	42.916
3	24.583	43.000	32.874
4	22.250	34.916	42.916
5	35.916	38.958	27.333
6	22.250	34.916	30.916
Mean	27.583	40.458	37.791
sd	5.1691	8.9959	7.2860
p value		0.0098	0.0215

- 20 **p value** refers to statistical significance when compared to unvaccinated controls.

Comment**ID-65 (3-60)**

5

Mice immunised with the '3-60 (ID-65)' DNA vaccine exhibited significantly longer survival times when compared with the unvaccinated control group.

ID-66 (3-5)

10

Mice immunised with the '3-5 (ID-66)' DNA vaccine exhibited significantly longer survival times when compared with the unvaccinated control group.

Example 3**15 Expression and Screening Group B Streptococcal LEEP derived Proteins in Protein vaccination experiments.****Expression of proteins**

20 Prioritised genes ie, those selected on the basis of predicted expression features as deduced from sequence characteristics (as described in Figure 1), were cloned and expressed as recombinant proteins using the pET system (Novagen, Inc., Madison, WI) utilising *Escherichia coli* as a host. Target genes were cloned into the pET28b(+) plasmid expression vector. The pET28b(+) vector is designed for high level expression and purification of target proteins. This vector carries a T7
25 promoter for transcription of a target gene, followed by an N-terminal His•Tag®/thrombin/T7•Tag® configuration, a multi-cloning site containing unique restriction enzyme sites for cloning purposes, and an optional C-terminal His•Tag sequence. The vector also carries a kanamycin resistance gene for selection purposes and for maintaining target gene expression (pET System Manual, 8th edition,
30 Novagen).

Preparation of protein vaccines

Oligonucleotide primers were designed for each individual target gene derived using the LEEP system unless stated otherwise. Each gene was examined thoroughly. Where possible primers were designed so that they would target that part of the gene predicted to encode only the mature portion of the protein (APPENDIX II). It is hoped that expressing those corresponding to the predicted mature protein only, might facilitate its correct folding when finally expressed *in vitro*. Oligonucleotide primers were designed so that sequences, encoding the putative N-terminal signal peptide of the target protein, would not be included in the final amplification product to be cloned pET28b(+). The signal peptide directs the polypeptide precursor to the cell membrane via the protein export pathway where it is normally cleaved off by signal peptidase I (or signal peptidase II if a lipoprotein). Hence the signal peptide would not be expected to form any part of the mature target protein, whether it be displayed on the bacterium's surface or secreted. For this purpose, classical signal peptides and their cleavage sites were predicted using the DNA Strider™ Program (CEA, France) and the SignalP V1.1 program, which predicts the presence and location of signal peptide cleavage sites in amino acid sequences from different organisms (Nielsen *et al.*, *Protein Engineering* 10: 1-6 (1997)). Where a N-terminal leader peptide sequence was not obvious, primers were designed to include the whole of the gene sequence for cloning and expression.

All oligonucleotide primers were designed to incorporate appropriate restriction enzyme sites to facilitate cloning into the pcDNA3.1 MCS region (APPENDIX II). Forward primers included an *Nco* I (5'-ccatgg-3') or *Nhe* I (5'-gctagc-3') restriction enzyme site and an 'ATG' start codon in-frame with the target gene open reading frame (orf). All reverse primers included a *Not* I restriction enzyme site 5' - gcggccgc-3' and were designed so that the target gene could be expressed in frame with the C-terminal His•Tag (i.e. the stop codon of the target gene was not

included). Using the *Nco* I and *Not* I, allowed the removal of the N-terminal His•Tag[®], thrombin and T7•Tag[®] DNA sequences. At the same time target genes were cloned immediately downstream of a highly efficient ribosome binding site (from the phage T7 major capsid protein), to facilitate high level
5 expression/translation of the target gene by T7 RNA polymerase, and subsequent purification by means of the C-terminal His•Tag. All target gene-specific forward and reverse primers were designed with compatible melting temperatures to facilitate their amplification.

All gene targets were amplified by PCR from *S. agalactiae* genomic DNA template
10 using Vent DNA polymerase (NEB) using conditions recommended by the manufacturer. A typical amplification reaction involved an initial denaturation step at 95°C for 2 minutes followed by 35 cycles of denaturation at 95°C for 30 seconds, annealing at the appropriate melting temperature for 30 seconds, and extension at 72°C for 1 minute (1 minute per kilobase of DNA being amplified). This was
15 followed by a final extension period at 72°C for 10 minutes. All PCR amplified products were extracted once with phenol:chloroform (2:1:1) and once with chloroform (1:1) and ethanol precipitated. Specific DNA fragments were isolated from agarose gels using the QIAquick Gel Extraction Kit (Qiagen). Purified target gene DNA amplicons were then digested *Nco* I (or *Nhe* I) and *Not* I restriction
20 enzymes, and cloned into *Nco* I and *Not* I digested pET28b(+) plasmid vector using *E. coli* DH5α or *E. coli* BL21 (DE3) as a host. Successful cloning and maintenance of genes was confirmed by restriction mapping.

Determination of target protein expression and solubility

25 Glycerol stocks of *E. coli* BL21 DE3 pET28b(+) strains expressing recombinant proteins were used to inoculate 10 ml Luria broth containing Kanamycin (30 µg/ml) which were grown overnight at 37°C with vigorous shaking (300 rpm).

A 20-40 ml Luria broth containing Kanamycin (30 μ g/ml) was inoculated with 1:100 dilution of the overnight culture from step 1 and grown at 37°C with vigorous shaking (300 rpm). When the culture reached an OD₆₀₀ of between 0.6 and 1.0, IPTG was added to a final concentration of 1mM. Typically cultures were induced for 3 hours. Cells were then harvested by centrifugation at 7000 g for 10 min. The cell pellet was then resuspended in 1/10 volume of lysis buffer (50mM NaH₂PO₄, pH.8.0; 300mM NaCl; 10mM imidazole; 10% glycerol). Lysozyme was then added to a final concentration of 1mg/ml, and the suspension was incubated on ice for 30 min. The suspension was then sonicated on ice (six 10-sec bursts at 200-300 W with a 10-sec cooling period). The lysate was then centrifuged at 10,000g for 20 min. The supernatant (containing soluble protein) was transferred to a sterile 2 ml eppendorf. The pellet was resuspended in 2 ml of solubilisation buffer (8 M Urea; 50mM NaH₂PO₄, pH.8.0; 300mM NaCl; 10% glycerol). This suspension contained the insoluble protein fraction. Aliquots from both the soluble and insoluble fractions were transferred to new eppendorfs. The protein samples were denatured by adding an equal volume of 2x SDS-PAGE buffer and heating at 95°C for 5 min. Denatured extract samples were then analysed by SDS-PAGE to determine target gene expression and solubility.

Large scale expression of recombinant target proteins

Glycerol stocks of *E. coli* BL21 DE3 pet28b(+) strains expressing recombinant proteins were used to inoculate 10 ml Luria broth containing Kanamycin (30 µg/ml) which were grown overnight at 37°C with vigorous shaking (300 rpm). 5 ml of an overnight culture of a recombinant strain was used to inoculate a 250 ml Luria broth containing kanamycin (30 µg/ml) which was grown at 37°C with vigorous shaking (300 rpm). When the culture reached an OD₆₀₀ of between 0.6 and 1.0, IPTG was added to a final concentration of 1mM. Typically, cultures were induced for 3 hours. Cultures were then centrifuged to a pellet and stored frozen at -20°C.

Purification of target antigens.

Ni-NTA agarose (Qiagen LTD, West Sussex, UK; Cat. No. 30210) was used to purify the His-Tagged recombinant proteins. The 6xHis affinity tag which was expressed in frame with the target proteins in pET28b(+), facilitates binding to Ni-NTA. Ni-NTA offers high binding capacity (with minimal non-specific binding) and can bind 5-10 mg of 6xHis-tagged protein per ml of resin. The 6xHis-tag is poorly immunogenic, and at pH 8.0, the tag is small, uncharged and therefore does not generally interfere with the structure and function of the protein (The QIAexpressionist, Qiagen Handbook, March 1999).

NOTE: All the proteins (LEEP-derived, unless stated otherwise) described here were purified under denaturing conditions except ID-65. ID-65 was prepared and purified under native conditions.

Purification under native conditions

The frozen pellet was allowed to thaw on ice for 15 minutes and then resuspended in 10 ml of lysis buffer (50mM NaH₂PO₄, pH.8.0; 300mM NaCl; 10mM imidazole;

10% glycerol). Lysozyme was then added to a final concentration of 1mg/ml, and the suspension was incubated on ice for 30 min. The suspension was then sonicated on ice (six 10-sec bursts at 200-300 W with a 10-sec cooling period). Dnase I (5 μ g/ml) was then added to the lysate, which was then incubated on ice for 10-15 min.

5 The lysate was then centrifuged at 10,000 rpm for 20 min at 4°C to pellet cell debris. The clear lysate supernatant was then loaded into a polypropylene column (Qiagen; Cat. No. 34964), bottom cap attached. 1.5 ml of 50% Ni-NTA was then added, the column sealed and the suspension was allowed to mix gently using a rotating wheel for 1-2 hours at 4°C. The column containing the lysate/Ni-NTA mix was then

10 placed upright using a retort stand, and the Ni-NTA was allowed to settle. The bottom cap was removed and the lysate was allowed to flow through. The column was then washed with three to six 4 ml volumes of wash buffer (50mM NaH₂PO₄, pH.8.0; 300mM NaCl; 20mM imidazole; 10% glycerol). The protein was then eluted in 0.5 ml aliquots of elution buffer (50mM NaH₂PO₄, pH.8.0; 300mM

15 NaCl; 500mM imidazole; 10% glycerol). Eluate fractions were then analysed by SDS-PAGE and those containing the protein were pooled and dialysed against a PBS (pH 7.0)-glycerol (10%) solution.

Purification and refolding under denaturing conditions

20

The frozen pellet was allowed to thaw on ice for 15 minutes and then resuspended in 10 ml of buffer containing 8 M Urea, 300 mM NaCl, 10% glycerol, 0.1 M NaH₂PO₄, pH.8.0, and 10 mM imidazole. The cells were then lysed by gentle vortexing for 1 hour at room temperature. The lysate was then centrifuged at

25 10,000g for 20 minutes to pellet cellular debris. The clear lysate supernatant was then loaded into a polypropylene column (Qiagen; Cat. No. 34964), bottom cap attached. 1.5 ml of 50% Ni-NTA slurry was then added, the column sealed and the suspension was allowed to mix gently using a rotating wheel for 1-2 hours at room

temperature. The column containing the lysate/Ni-NTA mix was then placed upright using a retort stand, and the Ni-NTA was allowed to settle. The bottom cap was removed and the lysate was allowed to flow through. The column was then washed with 4-8 ml of buffer containing 8 M Urea, 300 mM NaCl, 10% glycerol, 0.1 M NaH₂PO₄, pH 8.0, and 10 mM imidazole. The resin was then washed with a gradient of 6 to 0 M in a buffer containing 0.1 M NaH₂PO₄, pH 8.0, 300 mM NaCl and 10% glycerol to facilitate the slow removal of urea and gradual refolding of target protein. The resin was then washed with a buffer containing 0.1 M NaH₂PO₄, pH 7.0, 500 mM NaCl and 10% glycerol. The recombinant protein was then eluted in 0.5 ml aliquots with 500 mM Imidazole in 0.1 M NaH₂PO₄, pH 7.0, 500 mM NaCl and 10% glycerol. The fractions were analysed on SDS-PAGE and those containing the protein were pooled and dialysed against a PBS (pH 7.0)-glycerol (10%) solution.

All purified proteins were analysed by SDS-PAGE, as shown in Figures 5, 6 and 7, prior to their use as antigens in immunisation and vaccination experiments.

Protein Vaccinations

Vaccines were composed of the target protein in phosphate buffered saline/10% glycerol and mixed with aluminium hydroxide (alum) (Imject® Alum, Pierce, Rockford, Ill.). Each dose (unless otherwise stated) of vaccine contained 25 µg of purified protein in 50 µl of PBS/10% glycerol, mixed with 50 µl of alum. Groups of 6-8 CBA/ca mice (Harlan, UK) were immunised subcutaneously with the vaccines and again 4 weeks later. A control group received 100 µl dose of PBS/10% glycerol with alum. All vaccinated groups consisted of 6 mice. Mice were challenged at 7 weeks (unless otherwise stated). Mice were injected intraperitoneally (i.p.) with between 2.5-5 X 10⁶ bacteria diluted in 0.5 ml Todd-Hewitt broth. Deaths were recorded daily for 7 days. The challenged mice were observed daily for signs of illness. Typical symptoms in an appropriate order included piloerection, an

increasingly hunched posture, discharge from eyes, increased lethargy and reluctance to move which was often the result of apparent paralysis in the lower body/hind leg region. The latter symptoms usually coincided with the development of a moribund state at which stage the mice were culled to prevent further suffering. These mice were deemed to be very close to death, and the time of culling was used to determine a survival time for statistical analysis. Where mice were found dead, a survival time was calculated by averaging the time when a particular mouse was last observed alive and the time when found dead, in order to determine a more accurate time of death.

Analysis of antibody responses

Mice (6 per group) were immunised with two doses of vaccine with a four week interval. Mice were tail bled at 3 weeks and 6 weeks post primary vaccination to obtain sera. Total Immunoglobulin G (IgG) titres to the vaccine protein component in sera were determined by enzyme-linked immunosorbent assay (ELISA), using the original purified protein as the coating antigen.

Standard ELISA protocol

Solutions

Carbonate/bicarbonate buffer, pH 9.8

0.80g Na_2CO_3

1.46g NaHCO_3

pH to 9.6 using HCl

Add distilled water (dH_2O) to a final volume of 500ml.

p-NITROPHENYL PHOSPHATE SUBSTRATE

Diethanolamine Buffer, pH 9.8

48.5 ml diethanolamine

pH to 9.8 using 1M HCl

Add dH₂O to a final volume of 500ml

5

NOTE: ELISAs were optimised for each protein submitted for immunisation.

PROTOCOL

- 10 1. ELISA plates (Greiner labortechnik 96 well plates: Cat. No. 655061) with an appropriate concentration of recombinant protein diluted in carbonate/bicarbonate buffer (50 μ l/well). Cover plates with plastic or foil and leave overnight at 4°C.
2. Quickly wash plates twice in a tub/container containing PBS/0.05%Tween-20 and then pat dry.
- 15 3. Block plates with 3% BSA in PBS/Tween (100 μ l /well) for 1 hour at room temperature.
4. Wash the plates 3 times PBS/Tween as before and pat dry as before.
5. Apply (primary antibody) protein-specific antiserum (50 μ l/well) diluted from 1/50 in a doubling dilution series in PBS/Tween and incubate at room temperature for 90 minutes.
- 20 6. Wash plates as before (3 times quickly), followed up by 2 X 3 minute soaks (in PBS/Tween)
7. Apply diluted secondary antibody alkaline phosphatase conjugate. For anti-mouse Total IgG alkaline phosphatase conjugate (Goat Anti-Mouse IgG-AP, Southern Biotechnology Associates, Birmingham, AL. Cat. No. 1030-04) dilute 1/3000 in
25 PBS/Tween and apply 50 μ l per well and incubate at room temperature for 90 minutes.
8. Wash plates as in step 6.

9. Apply substrate. Dissolve one 5mg tablet of nitrophenyl phosphate (Sigma: kept in freezer) in 5ml of diethanolamine buffer. Apply 100 μ l per well. Cover with foil (a light-sensitive reaction) and leave at room temperature for 30 minutes. Read Optical densities (OD) at a wavelength of 405nm.
- 5 10. Plot curves of OD Vs dilution (log scale). Calculate end-point titres as the dilution giving the same OD as the mean of the OD obtained from the wells containing the 1/50 dilution of pre-immune serum.

10

15

ELISA Plate format

2°	1/50	1/10 0	1/20 0	1/40 0	1/80 0	1/160 0	1/32 00	1/640 0	1/ 1280 0	1/ 256 00	1/ 5120 0
1°	Duplicate										
Pre											
Pre											
Pre											

Table Summary

5 **Pre** Replicate wells of pooled pre-inoculation serum (50µl per well) diluted to 1/50 are included on every plate in order for end point titres to be calculated.

2° Is a blank control well to which no secondary antibody conjugate is applied. PBS/Tween by itself is applied instead

10 1° Is a blank control well to which no primary antibody is applied. PBS/Tween by itself is applied instead

Duplicate Each serum is analysed in duplicate

The dilution series used is indicated (see first row of table). Beginning with a 1/50 dilution, sera are diluted two-fold in PBS/Tween in doubling dilution series as indicated.

15

Protein Immunisation data**ID-65 and ID-83**

The ID-65 and ID-83 vaccines were composed of the target proteins in phosphate buffered saline/10% glycerol mixed with aluminium hydroxide (alum)

(Imject[®] Alum, Pierce, Rockford, Ill.). Each dose of vaccine contained 20 μ g of purified protein in 100 μ l of PBS/10% glycerol, mixed with 50 μ l of alum. A group of 6-8 week old CBA/ca mice (Harlan, UK) were immunised subcutaneously with the ID-65 and ID-83 vaccine and again 4 weeks later. A control group received a
5 150 μ l dose of PBS/10% glycerol (2:1) with alum. All groups consisted of 6 mice. Mice were tail bled at 5 weeks post primary vaccination to obtain sera. The presence of total Immunoglobulin G (IgG) antibodies to the ID-65 and ID-83 protein in sera was determined by enzyme-linked immunosorbent assay (ELISA), using the purified protein as the coating antigen. ELISA was also performed using sera obtained at 6
10 weeks post-primary vaccination from the PBS/10% glycerol immunised control group.

NOTE: ELISA plates were coated with the ID-65 or ID-83 proteins at a concentration of 1 μ g/ml.

15

Protein Vaccination -ELISA results for ID-65 and ID-83

Mice (6 per group) were immunised with two doses of the ID-65 and ID-83 vaccines with a four week interval. Mice were tail bled at 5 weeks post primary
20 vaccination to obtain sera. The Immunoglobulin G (IgG) titres to the vaccine protein component in sera were determined by enzyme-linked immunosorbent assay (ELISA), using the purified ID-65 and ID-83 proteins as the coating antigen. Subsequent to optimisation, ELISA plates were coated at a concentration 1 μ g/ml for both the purified ID-65 and ID-93 proteins. Total IgG titres were measured against
25 pre-immune serum (1/50 dilution). The results are shown in Table 2 and graphically in Figure 8.

30

Table 2

Serum (Group)	<u>ID-65 + Alum</u> (n=6)	<u>PBS + Alum</u> (n=6)	<u>ID-83 + Alum</u> (n=6)	<u>PBS + Alum</u> (n=6)
Coating antigen	<u>ID-65</u>		<u>ID-83</u>	
Bleed	<u>5 weeks</u>	<u>5 weeks</u>	<u>5 weeks</u>	<u>5 weeks</u>
<u>Total IgG Titres</u> (mouse 1-6)	7535763	965	82081	61
	1557649	90	50027	50
	3319737	108	154670	80
	1832259	176	57901	96
	8794360	371	66497	125
	1445728	0	49928	0
<u>Average</u>	4080916	285	76851	69
<u>Standard Deviation</u>	3258818	355	39985	43

5

Protein Immunisation and Challenge data (ID-93)**ID-93**

10 The ID-93 vaccine was composed of the target ID-93 protein in phosphate buffered saline/10% glycerol mixed with aluminium hydroxide (alum) (Imject® Alum, Pierce, Rockford, Ill.). Each dose of vaccine contained 25 µg of purified protein in 100 µl of PBS/10% glycerol, mixed with 100 µl of alum. A group of 6-8 week old CBA/ca mice (Harlan, UK) were immunised subcutaneously with the ID-93 vaccine and again 4 weeks later. A control group received PBS/10% glycerol with alum. Both

15 groups consisted of 6 mice. Mice were challenged at 7 weeks (unless otherwise stated). Mice were injected intraperitoneally (i.p.) with 5 X 10⁶ bacteria diluted in

0.5 ml Todd-Hewitt broth. The challenged mice were observed daily for signs of illness. Deaths were recorded daily for 7 days. Survival data are shown in Table 3 and graphically in Figure 9.

- 5 Mice were tail bled at 3 weeks and 6 weeks post primary vaccination to obtain sera. The presence of total Immunoglobulin G (IgG) antibodies to the ID-93 protein in sera was determined by enzyme-linked immunosorbent assay (ELISA), using the pure ID-93 protein as the coating antigen. ELISA was also performed using sera obtained at 6 weeks post-primary vaccination from the PBS/10% glycerol immunised control group.
- 10

Note: ELISA plates were coated with the ID-93 protein at a concentration of 1 $\mu\text{g/ml}$.

15 Table 3
ID-93 protein immunisation and GBS challenge experiment

Statistical analysis of Survival Times

Group	<u>PBS + Alum</u>	<u>ID-93 + Alum</u>
<u>Survival Times (hours)</u>	22.37	29.37
	22.37	35.12
	15.37	32.62
	28.03	32.62
	29.53	37.12
	26.53	27.87
Mean	24.03	32.45
sd	5.16	3.45
p value		0.01

20

p value refers to statistical significance when compared to unvaccinated controls.

Comment**5 ID-93 (RS-70)**

Mice immunised with the ID-93-Alum vaccine exhibited significantly longer survival times when compared with the PBS-Alum control group.

10 (Statistical Significance was determined by the Mann-Whitney U test using a 95% confidence level ($p > 0.05$)).

Protein Vaccination -ELISA results for ID-93

15 Mice (6 per group) were immunised with two doses of the ID-93 vaccine with a four week interval. Mice were tail bled at 3 weeks and 6 weeks post primary vaccination to obtain sera. The Immunoglobulin G (IgG) titres to the vaccine protein component in sera were determined by enzyme-linked immunosorbent assay (ELISA), using the purified ID-93 protein as the coating antigen. Subsequent to optimisation, ELISA plates were coated with the purified ID-93 protein at a concentration of 1 $\mu\text{g/ml}$.
20 Total IgG titres were measured against pre-immune serum (1/50 dilution). The results are shown in Table 4 and graphically in Figure 10.

Table 4

Serum Group	<u>ID-93 + Alum(n=6)</u>		<u>PBS/10%glycerol (n=6)</u> <u>(control)</u>	
Coating antigen	<u>ID-93</u>	<u>ID-93</u>	<u>ID-93</u>	<u>ID-93</u>
Bleed	<u>3 weeks</u>	<u>6 weeks</u>	<u>3 weeks</u>	<u>6 weeks</u>
<u>Total IgG</u> <u>Titres</u> <u>(mouse 1-</u> <u>6)</u>	87196	3000000	39	100
	99544	8000000	31	16
	19620	2000000	31	79
	34724	10000000	59	48
	59990	10000000	24	328
	30041	4000000	13	40
<u>Average</u>	55186	6166667	33	102
<u>Standard error</u>	32654	3600926	15	115

5

Protein Immunisation data ID-89 and ID-96

10 The ID-89 and ID-96 vaccines were composed of the target proteins in phosphate buffered saline/10% glycerol mixed with TitreMax Gold adjuvant (Sigma, Missouri, USA) according to the manufacturers instructions. The ID-89 vaccine contained 25 μ g of purified protein 50 μ l of PBS/10% glycerol, mixed with 50 μ l of TitreMax Gold. The ID-96 vaccine contained 12.5 μ g of purified protein 50 μ l of PBS/10% glycerol, mixed with 50 μ l of TitreMax Gold. Groups of 6-8 week old CBA/ca mice

15 (Harlan, UK) were immunised subcutaneously with the ID-89 and ID-96 vaccines and again 4 weeks later. A control group received a 100 μ l dose PBS/10% glycerol with TitreMax Gold (1:1). Both groups consisted of 6 mice. Mice were tail bled at 3

weeks and 6 weeks post primary vaccination to obtain sera. The presence of total Immunoglobulin G (IgG) antibodies to the ID-65 and ID-83 protein in sera was determined by enzyme-linked immunosorbent assay (ELISA), using the purified protein as the coating antigen. ELISA was also performed using sera obtained at 3 weeks and 6 weeks post-primary vaccination from the PBS/10% glycerol immunised control group.

Note: ELISA plates were coated with the ID-89 or ID-96 proteins at a concentration of 1 µg/ml and 3 µg/ml respectively.

Protein Vaccination -ELISA results for ID-89 and ID-96

Mice (6 per group) were immunised with two doses of the ID-89 and ID-96 vaccines with a four week interval. Mice were tail bled at 3 weeks and 6 weeks post primary vaccination to obtain sera. The Immunoglobulin G (IgG) titres to the vaccine protein component in sera were determined by enzyme-linked immunosorbent assay (ELISA), using the purified ID-65 and ID-83 proteins as the coating antigen. Subsequent to optimisation, ELISA plates were coated with purified ID-89 and ID-96 protein at a concentration 1µg/ml and 3 µg/ml respectively. Total IgG titres were measured against pre-immune serum (1/50 dilution). ELISA was also performed on both proteins using sera obtained at 3 weeks and 6 weeks post-primary vaccination from the PBS/10% glycerol immunised control group. Results are shown in tables 5a and 5b and graphically in Figure 11.

Table 5a

Serum	ID-89+TitreMax Gold (n=6)		ID-96+TitreMax Gold(n=6)	
Coating antigen	ID-89		ID-96	
Bleed	<u>3 weeks</u>	<u>6 weeks</u>	<u>3 weeks</u>	<u>6 weeks</u>
<u>Total IgG</u> <u>Titres</u> <u>(mouse 1-</u> <u>6)</u>	146940	1000000	190371	10000000
	89672	1000000	212505	10000000
	173532	2000000	167613	5000000
	85161	751210	110378	5000000
	88956	551281	142614	1000000
	27880	2000000	191085	1000000
Average	102024	1217082	169094	5333333
Standard Deviation	51451	629364	37341	4033196

Table 5b

Serum	<u>PBS/10%glycerol (n=6)</u>		<u>PBS/10%glycerol (n=6)</u>	
Coating protein	<u>ID-89</u>		<u>ID-96</u>	
Bleed	<u>3 weeks</u>	<u>6 weeks</u>	<u>3 weeks</u>	<u>6 weeks</u>
<u>Total IgG Titres (mouse 1-6)</u>	3	7	33	31
	8	18	77	62
	29	31	77	1
	34	4	52	29
	0	2	125	31
	5	1	113	0
Average	13	11	80	26
Standard deviation	15	12	35	23

Example 4**Conservation and variability of candidate vaccine antigen genes among different isolates of Group B Streptococci**

An initial Southern blot analysis was carried out to determine cross-serotype conservation of novel Group B Streptococcal genes isolated using the LEEP system unless stated otherwise. Analysing the serotype distribution of a target gene will also determine their potential use as antigen components in a GBS vaccine. The Group B Streptococcal strains whose DNA was analysed as part of this study are listed in APPENDIX III

Amplification and labelling of specific target genes as DNA probes for Southern blot analysis.

Oligonucleotide primers were designed for each individual gene of interest derived using the LEEP system unless stated otherwise. The same primers already described in APPENDIX II were used to amplify corresponding gene-specific DNA probes. Specific gene targets were amplified by PCR using Vent DNA polymerase (NEB) according to the manufacturers instructions. Typical reactions were carried out in a 100 μ l volume containing 50 ng of GBS template DNA, a one tenth volume of enzyme reaction buffer, 1 μ M of each primer, 250 μ M of each dNTP and 2 units of Vent DNA polymerase. A typical reaction contained an initial 2 minute denaturation at 95°C, followed by 35 cycles of denaturation at 95°C for 30 seconds, annealing at the appropriate melting temperature for 30 seconds, and extension at 72°C for 1 minute (1 minute per kilobase of DNA being amplified). The annealing temperature was determined by the lower melting temperature of the two oligonucleotide primers. The reaction was concluded with a final extension period of 10 minutes at 72°C.

All PCR amplified products were extracted once with phenol chloroform (2:1:1) and once with chloroform (1:1) and ethanol precipitated. Specific DNA fragments were isolated from agarose gels using the QIAquick Gel Extraction Kit (Qiagen). For use as DNA probes, purified amplified gene DNA fragments were labelled with digoxigenin using the DIG Nucleic Acid Labelling Kit (Boehringer Mannheim) according to the manufacturer's instructions.

Southern blot hybridisation analysis of Group B Streptococcal genomic DNA

Genomic DNA had previously been isolated from all strains of Group B Streptococci which were investigated for conservation of LEEP-derived (unless stated otherwise) gene targets. Appropriate DNA concentrations were digested using either *Hin* DIII or *Eco* RI restriction enzymes (NEB) according to manufacturer instructions and analysed by agarose gel electrophoresis. Following agarose gel electrophoresis of DNA samples, the gel was denatured in 0.25M HCl for 20 minutes and DNA was transferred onto Hybond™ N⁺ membrane (Amersham) by overnight capillary blotting. The method is essentially as described in Sambrook *et al.* (1989) using Whatman 3MM wicks on a platform over a reservoir of 0.4M NaOH. After transfer, the filter was washed briefly in 2x SSC and stored at 4°C in Saran wrap (Dow chemical company).

Filters were prehybridised, hybridised with the digoxigenin labelled DNA probes and washed using conditions recommended by Boehringer Mannheim when using their DIG Nucleic Acid Detection Kit. Filters were prehybridised at 68°C for one hour in hybridisation buffer (1% w/v supplied blocking reagent, 5x SSC, 0.1% v/v N-lauryl sarcosine, 0.02% v/v sodium dodecyl sulphate[SDS]). The digoxigenin labelled DNA probe was denatured at 99.9°C for 10 minutes before being added to the hybridisation buffer. Hybridisation was allowed to proceed overnight in a rotating Hybaid tube in a Hybaid Mini-hybridisation oven. Unbound probe was removed by washing the filter twice with 2x SSC- 0.1% SDS for 5 minutes at room

temperature. For increased stringency filters were then washed twice with 0.1x SSC-0.1% SDS for 15 minutes at 68°C. The DIG Nucleic Acid Detection Kit (Boehringer Mannheim) was used to immunologically detect specifically bound digoxigenin labelled DNA probes.

5

Results of Southern blot analysis

Unless otherwise stated, all genomic digests and their corresponding Southern blots followed an identical lane order as described in Table 6 below.

10

Table 6

Lane	1	2	3	4	5	6	7
Strain	1 kb molecular	515	A909	SB35	H36B	18RS21	1954/92
Serotype	Weight Marker	Ia	Ia	Ib	Ib	II	II

Lane	8	9	10	11	12	13	14
Strain	118/158	97/0057	BS30	M781	97/0099	3139	1169-NT
Serotype	II	II	III	III	III	IV	V

Lane	15	16	17	18	19	20
Strain	GBS 6	7271	JM9	Group A Streptococcus	<i>Streptococcus pneumoniae</i>	1 kb molecular
Serotype	VI	VII	VIII	—	14	Weight Marker

15

For comparative purposes, it was decided to analyse the serotype distribution of the GBS *rib* gene, which encodes the known protective immunogen Rib. Rib has previously been shown to be present in serotype III and some strains of serotype II but not in serotypes Ia or Ib (Stalhammar-Carlemalm *et al.*, *J. Exp. Med.* 177: 1593-1603 (1993)).

Confirmation of this pattern would not only give increased confidence in interpreting subsequent results, it would also determine if a *rib* gene homologue was present in the remaining GBS serotypes being investigated here. Primers designed for the amplification of *rib* for use as a gene probe in Southern blot analysis are described in APPENDIX II.

Table 7 – Lane order for Figure 12 (*rib* gene Southern blot analysis)

Lane	1	2	3	4	5	6	7
Strain	1 kb molecular weight marker	515	A909	SB35	H36B	18RS21	1954/92
Serotype		Ia	Ia	Ib	Ib	II	II

Lane	8	9	10	11	12	13	14
Strain	118/158	97/0057	BM110	BS30	M781	97/0099	3139
Serotype	II	II	III	III	III	III	IV

Lane	15	16	17	18	19	20
Strain	1169-NT	GBS 6	7271	JM9	Group A Streptococcus	<i>Streptococcus pneumoniae</i>
Serotype	V	VI	VII	VIII	—	14

Rib (Figure 12) Comment

5 The Southern blot analysis shown in Figure 12 indicates that the *rib* gene is not conserved across all GBS serotypes. *rib* appears to be absent from all serotype Ia and Ib strains (lanes 2 to 5) and from strains 118/158 and 97/0057 of serotype II (lanes 8 and 9). However, *rib* would appear to present in strains 18RS21 and 1954/92 of serotype II (lanes 6 and 7) and in all strains of serotype III (lanes 10 to 13). This is in agreement with previously published data (Stalhammar-Carlén *et al.*, 1993 [*supra*]). *rib* would also appear to be present in strains representing serotypes VII and VII (lanes 17 and 18) but was absent from strains representing serotypes IV, V and V (lanes 14 to 16) as well as the control strains (lanes 19 and 20). The *rib* gene probe did hybridise with lower intensity to genomic DNA fragments from strains representing serotypes Ia, Ib, IV, VI, VII and serotype II strains 118/158 and 97/0057. This may indicate the presence of a gene in these strains with a lower level of homology to *rib*. These hybridising DNA fragments may contain a homologue of the GBS *bca* gene encoding the Ca protein antigen which has been shown to be closely homologous to the Rib protein (Wastfelt *et al.*, *J. Biol. Chem.* 271:18892-18897 (1996)). If this is the case, it would be in agreement with previous work which showed all strains of serotypes Ia, Ib, II and III to be positive for one the two proteins (Stalhammar-Carlén *et al.*, 1993 [*supra*]). However, the apparent variable distribution of the *rib* gene amongst different GBS

serotypes, makes it a less than ideal candidate for use in a GBS vaccine that is cross-protective against all serotypes.

5

ID-65 (Figure 13) Comment

The Southern blot analysis described in Figure 13 indicates that gene ID-65 is conserved across all GBS serotypes. The gene probe hybridised specifically to a *Hin* DIII-digested genomic DNA fragment of approximately 3.0 kb in DNA digests from all GBS representatives, and was absent from both the control strains (lanes 18 and 19). This would suggest that the ID-65 gene is conserved across all GBS serotypes (and strains) at both the gene and locus level. The ID-65 DNA probe also hybridised weakly to the 1.636 bp molecular weight marker (the 1 kb DNA ladder from NEB was used to estimate DNA fragment sizes in all Southern blot analyses).

15

ID-89 (Figure 14) Comment

The Southern blot analysis described in Figure 14 indicates that gene ID-89 may not be conserved across all GBS serotypes. A 4.0 kb *Hin*DIII-digested genomic DNA fragment from 12 out of 16 GBS strains hybridised specifically to the ID-89 gene probe. In addition, a 3.25 kb *Hin*DIII-digested genomic DNA fragment from the GBS strain Ib (SB35) [lane 4] also hybridised specifically with the ID-89 gene probe. However, the ID-89 gene probe did not hybridise to digested genomic DNA fragments from strains Ia (515) [lane 2], IV (3139) [lane 13] and V (1169-NT) [lane 14], suggesting that these strains do not possess a ID-89 gene homologue.

20

ID-93 (Figure 15) Comment

The Southern blot analysis described in Figure 15 indicates that gene ID-93 is conserved across all GBS serotypes. The gene probe hybridised specifically to a *Hin*

25

DIII-digested genomic DNA fragment of approximately 3.25 kb in DNA digests from all GBS representatives, and was absent from both the control strains (lanes 18 and 19). This would suggest that the ID-93 gene is conserved across all GBS serotypes (and strains) at both the gene and locus level.

5

ID-96 (Figure 16) Comment

The Southern blot analysis described in Figure 16 indicates that gene ID-96 is conserved across all GBS serotypes. The gene probe hybridised specifically to a *Eco* RI-digested genomic DNA fragment of approximately 12.0 kb in DNA digests from all GBS representatives, and was absent from both the control strains (lanes 18 and 19). This would suggest that the ID-96 gene is conserved across all GBS serotypes (and strains) at both the gene and locus level.

10

APPENDIX I**ID-65**

Forward Primer

5 5' - cggatccgccaccatgGCGGATCAA~~A~~CTACATCGGTTC - 3'

Reverse Primer

5' - ttgcggccgcGTTGGGATAACTAGTCGGTTTAGTCG

Length (including restriction sites) = 1541bp

10 Incorporating 1515bp of gene-specific sequence encoding 505 amino acids of the putative mature protein.

Annealing temperature for PCR amplification = 60°C

Sequence predicted to encode a signal peptide was omitted from amplified product

15 **ID-66**

Forward Primer

5' - cggatccgccaccatgAATCTTTATTTCATAGTACTCCCTTGC - 3'

Reverse Primer

5' - ttgcggccgcAAAATGATCAGTTTGAGGGTAAAAGAG - 3'

20

Length (including restriction sites) = 767bp

Incorporating 747bp of gene-specific sequence encoding 247 amino acids of the putative mature protein.

Annealing temperature for PCR amplification = 60°C

25 Sequence predicted to encode a signal peptide was omitted from amplified product

APPENDIX II

ID-65

Forward Primer

5' - catgccatgGCGGATCAAACCTACATCGGTTC - 3'

5 Reverse Primer

5' - ttgcggccgcGTTGGGATAACTAGTCGGTTTAGTCG

Length (including restriction sites) = 1534bp

10 Incorporating 1515bp of gene-specific sequence encoding 505 amino acids of the putative mature protein.

Annealing temperature for PCR amplification = 60°C

ID-83

15 Forward Primer

5' - catgccatggcaAAAATAGTAGTACCAGTAATGCCTC - 3'

ReversePrimer

5' - ttgcggccgcCTCTGAAATAGTAATTTGTCCG - 3'

20 Length (including restriction sites) = 626bp

Incorporating 624bp of gene-specific sequence encoding 208 amino acids of the putative mature protein.

Annealing temperature for PCR amplification = 52°C

25

ID-89

Forward Primer

5' - catgccatgggaAAGAAAGCAAATAATGTCAGTCC - 3'

Reverse Primer

5' - ttgcggccgcATTGGGTGTAAGCATTTTTTC -3'

Length (including restriction sites) = 990bp

Incorporating 969bp of gene-specific sequence encoding 323 amino acids of the putative mature protein.

Annealing temperature for PCR amplification = 54°C

ID-93**Forward Primer**

10 5' - catgccatgggaACTGAGAACTGGTTACATACTAAAG - 3'

ReversePrimer

5' - ttgcggccgcATTAGCTTTTTCAACAATTTCTC - 3'

Length (including restriction sites) = 759bp

15 Incorporating 744bp of gene-specific sequence encoding 248 amino acids of the putative mature protein.

Annealing temperature for PCR amplification = 51°C

ID-96

20 **Forward Primer**

5' - ctagctagccgATGTTTGCGTGGGAAAG - 3'

ReversePrimer

5' - ttgcggccgcATAAGATTTAACAATACCAAGTAATATAGC - 3'

Length (including restriction sites) = 944bp

25 Incorporating 921bp of gene-specific sequence encoding 307 amino acids of the putative mature protein.

Annealing temperature for PCR amplification = 53°C

rib (control)

Forward primer

5' - ggggtaccggccaccATGGCTGAAGTAATTTTCAGGAAGT -3'

5 Reverse primer

5' - cggaattccgTTAATCCTCTTTTTTCTTAGAAACAGAT

Length (including restriction sites) = 3559bp

10 Incorporating 3531bp of gene-specific sequence encoding 1177 amino acids of the mature protein.

Annealing temperature for PCR amplification = 55°C

APPENDIX III

15 Listed below are the details (serotype and strain designation) of Group B Streptococcus strains whose DNA was analysed for gene conservation

		SEROTYPE	STRAIN
20	Ia	515	
	Ia	A909	
	Ib	SB35	
	Ib	H36B	
	II	18RS21	
25	II	1954/92	
	II	118/158	
	II	97/0057	
	III	BM110	
	III	BS30	
30	III	M781	
	III	97/0099	
	IV	3139	

V	1169/NT
VI	GBS VI
VII	7271
VIII	JM9

5

A group A Streptococcal strain (serotype M1, strain NCTC8198) and *Streptococcus pneumoniae* (serotype 14) were also included in the analysis for control purposes.

CLAIMS

1. A Group B Streptococcus polypeptide or protein having a sequence selected
5 from those described in fig 1, or fragments or derivatives thereof.
2. Derivatives or variants of the proteins, polypeptides, and peptides as claimed
in claim 1 which show at least 50% identity to those proteins, polypeptides and
peptides claimed in claim 1.
10
3. A Group B Streptococcus polypeptide or protein, or derivative or variant
thereof, as claimed in claim 1 or claim 2 , which is isolated or recombinant.
4. A nucleic molecule comprising or consisting of a sequence which is:
15
 - (i) any of the DNA sequences set out in figure 1 herein or their RNA
equivalents;
 - (ii) a sequence which is complementary to any of the sequences of (i);
 - (iii) a sequence which codes for the same protein or polypeptide, as those
20 sequences of (i) or (ii);
 - (iv) a sequence which shows substantial identity with any of those of (i), (ii)
and (iii); or
 - (v) a sequence which codes for a derivative, or fragment of a nucleic acid
molecule shown in figure 1.
25
5. A vector comprising one or nucleic acid molecules as defined in claim 4.

6. A vector as claimed in claim 4 further comprising nucleic acid encoding any one or more of the following: promoters, enhancers, signal sequences, leader sequences, translation start and stop signals, DNA stability controlling regions, or a fusion partner.

5

7. The use of a vector as claimed in claim 5 or claim 6 in the transformation or transfection of a prokaryotic or eukaryotic host.

8. A host cell transformed with a vector as defined in claim 5 or claim 6..

10

9. A process for producing a Group B Streptococcus polypeptide or protein, or derivative or variant thereof, as claimed in claim 1 or claim 2, the process comprising expressing the polypeptide or protein in a host cell as claimed in claim 8.

15

10. An antibody, an affibody, or a derivative thereof which binds to one or more of the proteins, polypeptides, peptides, fragments or derivatives thereof, as defined in any one of claims 1 to 3.

20

11. An immunogenic composition comprising one or more of the proteins, polypeptides, peptides, fragments or derivatives thereof as defined in any one of claims 1 to 3.

25

12. An immunogenic composition as claimed in claim 11 wherein the proteins, polypeptides, peptides, or fragments or derivatives thereof include ID-65 or ID-83, ID-89, ID-93 or ID-96.

13. An immunogenic composition as claimed in claim 11 or claim 12 which is a vaccine.

14. An immunogenic composition comprising one or more of the nucleic acid sequences as defined in claim 4.
- 5 15. An immunogenic composition as claimed in claim 14 wherein the nucleic acid sequences include ID-65 or ID-66.
16. An immunogenic composition as claimed in claim 14 or claim 15 which is a vaccine.
- 10 17. Use of an immunogenic composition as defined in any one of claims 11 to 16 in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection.
- 15 18. A method of detection of Group B Streptococcus which comprises the step of bringing into contact a sample to be tested with at least one antibody, affibody, or a derivative thereof, as defined in claim 10.
- 20 19. A method of detection of Group B Streptococcus which comprises the step of bringing into contact a sample to be tested with at least one protein, polypeptide, peptide, fragments or derivatives as defined in any one of claims 1 to 3.
- 25 20. A method of detection of Group B Streptococcus which comprises the step of bringing into contact a sample to be tested with at least one nucleic acid molecule as defined in claim 4.
21. A kit for the detection of Group B Streptococcus comprising at least one antibody, affibody, or derivatives thereof as defined in claim 10.

22. A kit for the detection of Group B Streptococcus comprising at least one Group B Streptococcus protein, polypeptide, peptide, fragment or derivative thereof as defined in any one of claims 1 to 3.

5

23. A kit for the detection of Group B Streptococcus comprising at least one nucleic acid molecule as defined in claim 4.

10

24. A method of determining whether a protein, polypeptide, peptide, fragment or derivative thereof as defined in any one of claims 1 to 3 represents a potential anti-microbial target which comprises inactivating said protein and determining whether Group B Streptococcus is still viable.

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FIG. 1

ID-65

Clone 3-60

GTGTTTATGATGAAAAAAGGACAAGTAAATGATACTAAGCAA
TCTTACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAA
TTTTAGGGTCATTTCATAATGGTCACAAGTCCTGTTTTGCGGA
TCAAACCTACATCGGTTCAAGTTAATAATCAGACAGGCACTAG
TGTGGATGCTAATAATTCTTCCAATGAGACAAGTGCGTCAAGT
GTGATTACTTCCAATAATGATAGTGTTCAGCGTCTGATAAAG
TTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
CTTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTG
AACAAAGGAATTATGTTTATAGCAAAGAAACCGAGGTGAAAA
ATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAAAGAA
AGGTGATAAAGTTTTCTATGACCAAGTATTTAATAAAGATAAT
GTGAAATGGATTTTCATATAAGTCTTTTGGTGGCGTACGTCGAT
ACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAGA
CTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATC
AAGAGAAAATAGCAACGCAAGGAAATTATACATTTTCACATA
AAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAGTCCAACTC
AATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAAA
TACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAATCATT
CAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGCATCTTCA
GTAGAAAAAACTGAAGATAAAGAAAAAAGTGTCTCCTCAACCA
CAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACG
AAACAACCTACAGGTTTTGATATTTTAATTACGAATATTAAGA
TGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTGGACTGAA
CAAGGAGGGCAAGATGATATTAATGGTATACAGCTGTAACCT
ACTGGGGATGGCAACTACAAAGTAGCTGTATCATTGCTGAC
CATAAGAATGAGAAGGGTCTTTATAATATTCATTTATACTACC
AAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACCTAAAG
TGACAGTAGCTGGAACCTAATTCTTCTCAAGAACCTATTGAAAA
TGGTTTACCAAAGACTGGTGTATAATATTATCGGAAGTACT
GAAGTAAAAAATGAAGCTAAAATATCAAGTCAGACCCAATTT
ACTTTAGAAAAAGGTGACAAAATAAATTATGATCAAGTATTG
ACAGCAGATGGTTACCAAGTGGATTTCTTACAAATCTTATAGTG
GTGTTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAGTAG
TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCC
CAACTTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTA
GATGTGAAAAGTCAACCTAAAGTATCAAGTCCAGTGGAATTT
AATTTTCAAAAGGGTGAAAAAATACATTATGATCAAGTGTTA
GTAGTAGATGGTCATCAGTGGATTTTCATACAAGAGTTATTCCG
GTATTCGTCGCTATATTGAAATTTAA

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MFMMKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNN
QTGTSVDANSSNETSASSVITSNNDQSVQASDKVVNSQNTATKDITPLVETK
PMVEKTLPEQGNVYVYSKETEVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDN
VKWISYKSFGGVRRYAAIESLDPSGGSETKAPTPVTNSGSNNQEKIATQGNYT
FSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGNQWLSYKSFNGVRRFV
LLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFDILITNIKDDNGIA
AVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNIHLY
YQEASGTLVGVGTGKVTVAGTNSSQEPINGLPKTGVYNIIGSTEVKNEAKISS
QTQFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSEKAKDE
ATKPTSYPNLPKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHVDQVLVVD
GHQWISYKSYSGIRRYIEI*

Sequence description

A) Length: 1642 bp - 547 aa (full length gene)

B) Sequence Characteristics:

Potential leader peptide sequence

Orf is preceded by a potential Shine-

Dalgarno sequence.

ID-66

Clone 3-5

ATGATATTGAGACGTCGAACCTATTGTTTTATGGCAACTGGGTATCGCCATT
TCTCTCATTCTTAGTATTCTAGCCTTAAATCTTTATTTCCATAGTACTCCCTT
GCAAACCAATGCAGCTTTACGGAACCTTGCTCCTTCATTAAACCATCTTTTT
GGGACAGATGGTTTAGGTAGGGATATGTTTGTGACAACGATTAAAGGACT
TTATTTCTCTCTACAAGTCGGCTTATTAGGTGCCCTTATGGGGGTGATTCTG
GCGACAGTTTTTGGAGTGCTTGCAGGTTTAGGAAATAGCATTATTGATAAA
ATAATAGCATGGTTAGTTGATTGTTTATTGGTATGCCTCATTGATTTTAA
TGATTCTCATTCTTTTGTGTTGGGAAAGGTGCTCAAGGGGTGATCATTGC
AACGGCTGTTACACATTGGCCTTCTTTAGCAAGGCTTATCCGCAATGAAGT
CTATCATCTAAAGAATAAAGAATTTGTCCAACCTTTCTAAAAGTATGGGAAA
AACGCCTTATTATATTGTGAGGCATCATATCCTGCCTTTGATTGCTTCTCAA
ATTTTCATTGGTTTTATCCTCTTATTTCCACATGTCATCCTACATGAAGCAT
CAATGACTTTCTTAGGATTTGGGCTCTCTGCCGAACAACCTTCGGTTGGTA
TCATTCTGTGAGAGGCAGCTAAGCATATCTCTCTTGGAAATTGGTGGTTGG
TTATCTTTCCAGGACTTTATCTTATTTTGGTTGTCAATGCATTTGATACTAT
CGGAGAATCTTTAAAGAACTCTTTTACCCTCAAACCTGATCATTTTTAG

FIG. 1 CONT'D

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MILRRRTIVLWQLGIAISLILSILALNLYFHSTPLQTNAALRNLAAPSLNHLFGTD
 GLGRDMFVRTIKGLYFSLQVGLLGALMGVILATVFGVLAGLGNSIIDKIIAWL
 VDLFIGMPHLIFMILISFVVGKGAQGVIIATAVTHWPSLARLIRNEVYHLKNKE
 FVQLSKSMGKTPYYIVRHHILPLIASQIFIGFILLFPHVILHEASMTFLGFGLSAE
 QPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFYPQTDHF
 *

Sequence description

A) Length: 822 bp - 274 aa (full length gene)

B) Sequence Characteristics:

Potential leader peptide sequence

Orf is preceded by a potential Shine-

Dalgarno sequence.

ID-78

Clone 3-5b

ATGACAGAAACATTATTAAGCATTAAAGACCTCTCCATCACCTTCACTCAA
 TACGGAAGATTTTTAAAACCATTTCAATCAACACCGATACAAGCGCTGA
 ATTTAGAAATTAAAAAAGGTGAGTTATTAGCTATTATAGGTGCTAGTGTT
 CGGGGAAGAGTTTATTAGCACATGCTATTATGGATATTCTTCCTAAAAATG
 CATCTGTAACAGGAGATATGATTTATCGTGGTCAATCACTAAATTCTAAAC
 GCATTAAACAGTTGCGAGGAAAAGATATTACGTTGATTCCACAATCAGTTA
 ATTATTTAGATCCATCTATGAAAGTCAAACATCAGGTGCGCTTAGGTATCT
 CAGAAAATTCAAAGGCTACTCAAGAAGGATTGTTTCAACAGTTTGGTTTAA
 AAGAAAGTGATGGTGACTTGGATCCTTTCCAACCTTCTGGCGGAATGCTCC
 GACGTGTTTTGTTTACAACGTGTATTAGTGATAAGGTTTCTTTGATTATTGC
 GGATGAGCCCACCCCTGGATTACATCCAGATGCTCTGCAAATGGTTTTAGA
 CCAACTACGCTCCTTTGCAGATAAAGGAATAAGCGTTATATTTATCACTCA
 TGATATTGTAGCAGCTAGTCAAATTGCTGATCGTATTACTATTTTTAAAGA
 GGGAAAAGCTATTGAAACAGCTCCAGCTAGTTTCTTTAGCGGAAATGGAG
 AGCAGTTACAAACAGAATTTGCTAGAAGTTTATGGCGCTCTCTCCACAGC
 AAGAATTTTTGAAAGGAGTTACTCATGACCTTAGAGGCTAA

MTETLLSIKDLSITFTQYGRFLKPFQSTPIQALNLEIKKGELLAHIGASGSGKSL
 AHAIMDILPKNASVTGDMIYRGQSLNSKRIKQLRGKDITLIPQSVNYLDPSMK
 VKHQVRLGISENSKATQEGLFQQFGLKESDGDLPFQLSGGMLRRVLFTTCIS
 DKVSLIIADEPTPGLHPDALQMVLDQLRSFADKGISVIFITHDIVAASQIADRITI
 FKEGKAJETAPASFFSGNGEQLQTEFARSLWRS LPQGEFLKGVTHDLRG*

FIG. 1 CONT'D

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Sequence description

A) Length: 804 bp - 268 aa (full length gene)

B) Sequence Characteristics:

No obvious leader peptide sequence

Orf is preceded by a potential Shine-Dalgarno sequence.

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified downstream and fully sequenced.

ID-79

Clone 3-5c

GTCCATCTGGGGTGGTTCCCGATTGGTATTTCTTCTCCGATAGGTACTTTGA
 GTCAAGATATTACGTTAGCTGATCGTATTAAGCACCTTATTTTACCTGTTT
 CACGGTAAGTATTCTAGGCATTGCCAATGTAACCTCTTCATACTAGAACTAA
 AATGATGTCGGTACTTTCTAGTGAATATGTCTTATTTGCCAGAGCGCGTGG
 GGAAACGGAATGGCAAATTTTAAAAATCATTGTCTTAGAAATGCTATCGT
 ACCAGCTATTACACTGCATTTTTCCTATTTGGAGAATTGTTTGGAGGATCC
 GTTCTTGCTGAGCAAGTTTCTCATATCCAGGACTAGGGTCTACCCTAACT
 GAAGCAGGACTTAAAAGTGATACACCGCTACTTCTAGCTATTGTGATGATA
 GGGACATTATTTGTTTTGCGGGCAATCTTATTGCGGATATTTTAAATAGC
 ATAATCAATCCACAGTTAAGGAGAAAAGTATGA

VHLGWFPIGISSPIGTLSDITLADRIKHLILPVFTVSILGIANVTLHTRTKMMSV
 LSSEYVLFARARGETEWQIFKNHCLRNAIVPAITLHFSYFGELFGGSVLAEQVF
 SYPGLGSTLTEAGLKSDTPLLLAIVMIGTLFVFAGNLIADILNSIINPQLRRKV*

Sequence description

A) Length: 495 bp - 165 aa (partial gene sequence)

B) Sequence Characteristics:

N-terminus has yet to be determined.

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified upstream.

FIG. 1 CONT'D

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ID-80

Clone 2-17

TTGCGGACAATTACGTTCAAACACAATGAAACGCGATCGTCAAAAAGCGA
AGGTAGGGCGGTAATGCTTAAAAGATTATTTACTGAAGATGGGGAATTGA
CAAAGATTAGTCGTCGTTTCGTTTGGATGTTAGTGGTTATCTATTGTCTTAT
TATTGTCAGGATGTGTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAAC
TCCGAATGTTTCAGCGCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTTAA
TTCTTTTCGTAGTTTAGATCAGCTAACTAGCTTTAAAGAGATTTTTTGGGTT
ATTGGTCAAAATGTAGTGAATATTTTACTGCTGTTTCCTCTCATTATAGGGT
TACTATCCCTAAAGCCAAGTTTACGGAAATATAAAAGCGTTATATTACTTG
CTTCTTGATGTCTCTTTTCATAGAGTGTACTCAAGTTGTTTTAGATATTTT
AATAGATGCTAATCGGGTTTTTCAAATCGACGATCTATGGACAAATACCTT
AGGCGGTCCTTTCGCCCTATGGAGTTATCGAAACATAAAAGGTTGGCTTCT
AACTATTAGAAAATGA

MRTITFKHNETRSSKSEGRAVMLKRLFTEDGELTKISRRFVWMLVVIYCLIIVR
MCFGQPIMIEGVSTPNVQRFGRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVV
NILLFLPLIIGLLSLKPSLRKYKSVILLAFLMSLFIECTQVVLDILIDANRVFEIDD
LWTNTLGGPFALWSYRNIKWLLTIRK*

Sequence description

- A) Length: 579 bp - 193 aa (full length gene)
- B) Sequence Characteristics:
 - Possesses a potential leader peptide sequence
 - No obvious Shine-Dalgarno, but the 'TTG' codon may not be the actual translation start point.
 - A methionine (ATG) that occurs ~22 codons downstream of the 'TTG' is preceded by a potential Shine-Dalgarno sequence and may represent the actual start codon.

ID 81

Clone 3-1

FIG. 1 CONT'D

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TTGAAAAATTTAAATCGTTATGTAGTTGCGGTTTCTGGAGTCGTTTTACATT
 TAATGCTAGGATCAACTTATGCTTGGAGTGTGTTTCGTAACCCAATTATCT
 CAGAGACTGGTTGGGATATTTTCATCAGTTTCATTTCGCTTTTAGTTTGGCTAT
 TTTTGTCTAGGAATGTCTGCAGCTTTTATGGGACACTTAGTAGAGCGTTTT
 GGTCCTAGGATAATGGGAATGATTTCTGCTATTTTATATGGAGCAGGGAAT
 GTGTTAACAGGCTTAGCCATTGAACTCAGCAGTTATGGTTACTGTATGTT
 GCATACGGTATTTTAGGAGGAATCGGACTTGGTTCAGGTTATATTACTCCA
 GTATCGACTATTATTAATGGTTTCCTGATAGGAGGGGACTAGCAACAGG
 ATTCGCTATTATGGGATTTGGCTTTGCTTCTTTAGTAACAAGTCCGCTTGCA
 CAATCCTTACTGATTAGGATTGGTGTGGGTAAAACGTTTTATATTTTGGGA
 TTAGTATATTTTTTGTTCATGATGATTGCCTCACAATTTATTAAACAACCAC
 CTCAGGAAAAAATAACTATTTTGA CTACGATGGTAAAAAGAATGCTATG
 AATTCACAAATTATCACTGGATTA AAAAGCAAACGTCGCTATAAAATCAAA
 AACCTTTTACATCATTGGTTGACCTTGTTTATTAATATTTTCGTGTGGCTTA
 GGTTTAATATCAGCAGCTTCACCAATGGCACAAGATTTAGCAGGCTATTCC
 GCAGAATCTGCAGCCTTATTAGTAGGGGTACTAGGGATATTTAACGGTTTT
 GGACGTCTGTTATGGGCAAGTCTCTCTGACTACATTGGACGCCCGTTGACC
 TTTATAATATTATTTATTGTGAACCTTATTATGACTTCTAGTTTATTTTTGTC
 ATTCAATGCTATTGTATTTGCAATAGCGATGTCTATTTTAATGACTTGTTAT
 GGTGCAGGTTTTTTCCTTATTACCTGCTTATCTAAGTGATATTTTGGAAACAA
 AGGAATTAGCTACTTTACATGGTTATAGTTTAACAGCATGGGCAATAGCAG
 GTCTGTTTGGGCCCTTATTGTTATCAAAGACATATTCATGGGGAAATTCCT
 ATCAATTGACATTAATGGTTTTTGGTTTTTTATTCTTATTCGGATTATTGTTA
 TCTCTATATTTAAGAAAATTAACA ACTAAAGTTGTGTAG

LKNLNRYVVA VSGVVLHMLGSTYAWSVFRNPIISETGWDISSVSFAFSLAIFC
 LGMSAAFMGHLVERFGPRIMG MISAILYGAGNVLTGLAIETQQLWLLYVAYG
 ILGGIGLGSYITPVSTIWKWFPDRRGLATGFAIMGFGFASLVTSPLAQSLIRIG
 VGKTFYILGLVYFFVMMIASQFIKQPPQEKITILTHDGKKNAMNSQIITGLKAN
 VAIKSKTFYIIWLT LFINISCGLGLISAASPM AQDLAGYSAESAALLVGVLGIFN
 GFGRLLWASLSDYIGRPLTFIILFIVNFIMTSSLFSLFNAIVFAIAMSILMTCYGA
 GFSLLPAYLS DIFGTELATLHGYSLTAWA IAGLFGPLLLSKTYSWGNSYQLTL
 MVFGFLFLGLLLSLYLRKLTTKV*

Sequence description:

- A] Length 1221 bp - 407 a.a (full length gene).
- B] TTG start codon with Shine-Dalgarno sequence upstream. Obvious signal peptide, with hydropathy plot exhibiting many possible membrane spanning regions, indicating protein to be transmembrane.

FIG. 1 CONT'D

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ID-82

Clone 48

ATGGCAGATAAAAAACAGAACATTTAACTTGTAGGTGCAGGATCTTCTAG
CACACAAGAAAAAATTGAAAAGCCTGCTCTTTTCGTTTATGCAAGATGCGTG
GCGTCGCTTGAAAAAAAACAAATTAGCAGTAGTTTCACTCTATTTATTAGC
TCTTTTACTTACTTTTTTCGTTAGCCTCAAATTTATTTGTAACCTCAGAAGGAT
GCTAATGGGTTTGATTTCGAAAAAAGTAACGACATATCGCAACTTACCACCT
AAATTGAGTTCAAACCTTCCTTTTTGGAATGGTAGCATTAAATCCATCA

MADKNRTFKLVGAGSSSTQEKIEKPALSFMQDAWRRLKKNKLAVVSLYLLA
LLTFSLASNLFVTQKDANGFDSKKVTTYRNLPPKLSSNLPFWNGSINPS

Sequence description:

A] Current length is 303 bp - 101 aa
B] No obvious signal peptide but Shine
Dalgarno sequence upstream of the ATG start
codon. Not identified directly using the LEEP system but was found
directly downstream of ID-34 described in WO 00/06736.

ID-83

Clone 98

ATGAAAATAGTAGTACCAGTAATGCCTCGCAGTCTTGAAGAGGCTCAAGA
AATAGATTTATCAAAATTTGATAGTGTTGATATTATTGAATGGCGAGCTGA
TGCCTTACCAAAGGATGACATTATTAATGTAGCTCCAGCTATTTTTGAGAA
ATTCGCAGGTCATGAAATTATTTTTACTTTTCGTACAACGCGTGAAGGTGG
TAATATTGTCTTATCTGATGCTGAGTATGTTGAGTTAATCCAGAAAATTAA
TTCTATCTACAATCCAGATTATATTGATTTTGAGTATTTTTACATAAAGAA
GTTTTTCAAGAAATGCTAGAATTTCCAAATTTAGTCCTGTCTTATCACAATT
TTCAAGAGACACCGGAGAATATTATGGAGATATTTTCAGAATTAACAGCC
CTAGCACCACGAGTTGTGAAAATCGCAGTAATGCCAAAGAATGAACAAGA

FIG. 1 CONT'D

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TGTCTTAGACGTTATGAATTACACTCGCGGTTTCAAGACTATTAATCCTGA
TCAAGTTTATGCGACGGTATCTATGAGTAAAATTGGACGATTTTCTCGTTTT
GCTGGTGATGTAAGTGGATCTAGTTGGACATTTGCATATTTAGATTCATCT
ATCGCACCCGGACAAATTACTATTTTCAGAGATGAAGCGTGTCAAAGCATT
GCTTGACGCTGACTGA

MKIVVPVMPRSLEEAQEIDLSKFDSVDIIEWRADALPKDDIINVAPAIFEK FAG
HEIIFTFRTTREGGNIVLSDAEYVELIQKINSIYNPDYIDFEYFSHKEVFQEMLEF
PNLVLSYHNQFETPENIMEIFSELTAAPRVVKIAVMPKNEQDVLDVMNYTRG
FKTINPDQVYATVSMKIGRISR FAGDVTGSSWTFAYLDSSIAPGQITISEMKRV
KALLDAD*

Sequence description:

- A] Length 678 bp, 225 aa (full length gene)
- B] No obvious signal peptide, but there is a
Shine Dalgarno immediately upstream of ORF.

ID-84

Clone RS-52

ATGAAAGACTTATTTGCAACAACAGAAGCATCATCAAGGAAACAGGAACA
AGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAACAATGGTA
ATCAAATAAAAAAATTGAGTTTATCGACTTTCAAAAAATGAGATGACA
GGTACATGGGGAATTTCTACTAAAATTAATGAACAATTTTCGATTAGTTTT
TCTGAAGATAGAATTGGTGGTAACTTAGAGCATTAGGATATCAACCGAA
TGAAATAGGTTTTTCAAAGGACATCAATAGTAATAATCAAAATGTTAATGA
TATTGAAGTGATTTATATGAAGAAAGAATAG

MKDLFATTEASSRKQEQDRIVNYIKQHVELTNGNQIKKIEFIDFQKNEMTGTW
GISTKINEQFSISFSEDRIGGKLRALGYQPNEIGFSKDINSNNQNVNDIEVIYMK
KE*

Sequence description:

- A] length: 333 bp - 111 aa (partial sequence)
- B] No obvious Shine Dalgarno sequence upstream
of the ATG start codon, and no obvious signal
peptide within the protein.

FIG. 1 CONT'D

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ID-85

Clone RS-53

ATGAAAAAACGTATATGGTATTTGATAATAATAATCACAGTAATTTTAGGA
GGACTAGCCATGAAAAACTTATTTGCAACAACAGAAGCATCATCAAGGAA
ACAGGAACAAGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAA
CAAATGGTAATCAAATAAAAAAAATTGAGTTTATCGACTTTCAAAAAAAT
GAGATGACAGGTACATGGGGAATTTCTACTAAAATTAATGAACAATTTTCG
ATTAGTTTTTCTGAAGATAGAATTGGTGGTAAACTTAGAGCATTAGGATAT
CAACCGAATGAAATAGGTTTTTCAAAGGACATCAATAGTAATAATCA

MKKRIWYLIHITVILGGLAMKNLFATTEASSRKQEQRIVNYIKQHVELTNGN
QIKKIEFIDFQKNEMTGTWGISTKINEQFSISFSEDRIGGKLRLALGYQPNEIGFSK
DINSNNQ

Sequence description:

- A) Length: 351 bp - 117 aa (Partial sequence)
B) Obvious signal peptide and Shine Dalgarno
sequence upstream of the ATG start codon.

ID-86

Clone ID-74

ATGTCAAATCAATATGATTATATCGTTATTGGTGGAGGTAGT
GCAGGCAGTGGTACCGCTAATAGGGCAGCCATGTATGGAGC
AAAAGTCCTGTTAATTGAAGGTGGACAAGTAGGTGGAACCTG
TGTTAACTTAGGTTGTGTACCTAAGAAAATCATGTGGTATGG
TGCACAAGTTTCTGAGACACTCCATAAGTATAGTTCAGGTTA
TGGTTTTGAAGCCAATAATCTTAGTTTTGATTTTACTACTCTA
AAAGCTAATCGCGATGCTTACGTGCAGCGGTCTAGACAGTCG
TATGCCGCTAATTTTGAGCGTAATGGGGTCGAAAAGATTGAT
GGATTTGCTCGTTTTATTGATAACCATACTATTGAAGTGAATG
GTCAGCAATATAAAGCTCCTCACATTACTATTGCAACAGGTG

FIG. 1^{CONT'D}

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GACACCCTCTTTACCCTGATATTATTGGAAGTGAACCTTGGTG
AGACTTCTGATGATTTTTTTGGATGGGAGACCTTACCAAATTC
TATATTGATTGTTGGGGCGGGCTATATCGCGGCAGAACTTGC
TGGAGTGGTTAATGAATTAGGCGTTGAAACCCATCTTGCATT
TAGAAAAGACCATATTCTACGCGGATTTGATGACATGGTAAC
AAGTGAGGTTATGGCTGAAATGGAGAAATCAGGTATCTCTTT
ACATGCTAACCATGTACCTAAATCTCTTAAACGCGATGAAGG
TGGCAAGTTGATTTTTGAAGCTGAAAATGGGAAAACGCTTGT
CGTTGATCGTGTAATATGGGCTATCGGCCGTGGACCAAATGT
AGACATGGGACTTGAAAATACCGATATTGTTTTAAATGATAA
AGATTATATCAAAACAGATGAATTTGAGAATACTTCTGTAGA
TGGCGTGTATGCTATTGGAGATGTTAATGGGAAAATTGCCTT
GACACCGGTAGCAATTGCAGCAGGTCGTCGCTTATCAGAAAG
ACTTTTTAATCATAAAGATAACGAAAAATTAGATTACCATAA
TGTACCTTCAGTTATTTTTACTCACCCTGTAATTGGGACGGTA
GGACTTTCAGAAGCAGCAGCTATCGAGCAATTTGGAAAAGAT
AATATCAAAGTCTATACATCAACTTTTACCTCTATGTATACGG
CTGTTACCAGTAATCGCCAAGCAGTTAAGATGAAGCTCATAA
CCCTAGGAAAAGAGGAAAAAGTTATTGGGCTTCATGGTGTTG
GTTATGGTATTGATGAAATGATTCAAGGTTTTTCAGTTGCTAT
CAAAATGGGGGCTACTAAAGCAGACTTTGATGATACTGTTGC
TATTCACCCAACCTGGATCTGAGGAATTTGTTACAATGCGCTA
A

MSNQYDYIVIGGGSAGSGTANRAAMYGAKVLLIEGGQVGGTC
VNLGCVPKKIMWYGAQVSETLHKYSSGYGFEANNLSFDFTTLK
ANRDAYVQRSRQSYAANFERNGVEKIDGFARFIDNHTIEVNGQ
QYKAPHITATGGHPLYPDIIGSELGETSDDFFGWETLPNSILIVG
AGYIAAELAGVVNELGVETHLAFRKDHILRGFDDMTSEVMAE
MEKSGISLHANHVPKSLKRDEGGKLIFEANGKTLVVDRVIWAI
GRGPNVDMGLENTDIVLNDKDYIKTDEFENTSVDGVYAIGDVN
GKIALTPVAIAAGRRLSERLFNHKDNEKLDYHNVPSVIFTHPVIG
TVGLSEAAAIEQFGKDNKIVYTSTFTSMYTAVTSNRQAVKMKLI
TLGKEEKVIGLHGVGYGIDEMIQGFSVAIKMGATKADFDDTVAI
HPTGSEEFVTMR*

ID-87

FIG. 1 CONT'D

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Clone RS-55

ATGACAAAAAACATCTTAAAAACGCTTGCCTTGGCACTTACTACAGTATCA
GTAGTGACATACAGCCAGGAGGTATATGGATTAGAAAGAGAGGAATCGGT
CAAACAAGAACAAACCCAGTCAGCTTCAGAAGATGATTGGTTCGAAGAAG
ATAATGAGAGGAAAAACAATGTTTCTAAAGAGAATTCTACTGTTGATGAA
ACAGTTAGTGATTTATTTTCTGATGGAAATAGTAATAACTCTAGTTCTAAA
ACCGAGTCAGTGGTAAGTGACCCTAAACAAGTCCCCAAAGCAAAACCAGA
GGTTACACAAGAAGCAAGCAATTCTAGTAATGATGCTAGCAAAGTAGAAG
TACCAAAACAGGATACAGCTTCAAAAAAGGAACTCTAGAAACATCAACT
TGGGAGGCAAAAGATTTTCGTAAGTACAGGGGATACTTTAGTAGGTTTTTCA
AAATCTGGAATTAATAAGTTATCTCAAACATCACACTTGGTTTTACCAAGT
CATGCAGCAGATGGAAGTCAATTGACACAAGTAGCTAGCTTTGCTTTTACT
CCAGATAAAAAGACGGCCATTGCAGAATATACAAGTAGGCTAGGAGAAA
ATGGGAAACCGAGTCGTTTAGATATTGATCAGAAGGAAATTATTGATGAG
GGAGAAATATTTAATGCTTACCAGTTGACTAAGCTTACTATTCCAAATGGT
TATAAGTCTATTGGTCAAGATGCTTTTGTGGACAATAAGAATATTGCTGAG
GTTAACCTTCTGAGAGTCTCGAGACTATTTTCAGACTATGCTTTTGTCTACA
TGTCTTTAAACAAGTAAAGTTACCAGATAACCTAAAGGTCATTGGAGAA
TTAGCTTTTTTTGATAATCAGATTGGTGGTAAGCTTTACTTGCCACGTCCT
TGATAAAATTAGCAGAACGCGCTTTCAAATCTAATCGTATTCAAACAGTTG
AATTTTTGGGAAGTAAGCTTAAGGTTATAGGAGAAGCAAGTTTTCAAGAT
AATAATCTGAGGAATGTTATGCTTCCGGATGGACTTGAAAAAATAGAATC
AGAAGCTTTTACAGGAAATCCAGGAGATGAACATTACAACAATCAGGTTG
TATTGCGCACAAGGACAGGCCAAAATCCACATCAACTTGCGACTGAGAAT
ACTTACGTCAATCCGGACAAATCATTGTGGCGTGCAACACCTGATATGGAT
TATACCAAATGGTTAGAGGAAGATTTTACCTATCAAAAAAATAGTGTTACA
GGTTTTTCAAATAAAGGCTTACAAAAGGTAAGACGTAATAAAAACTTAGA
AATCCAAAACAACACAATGGTATTACTATTACTGAAATTGGTGATAACGC
TTTTTCGCAATGTTGATTTTCAAAGTAAACTTTACGTAAATATGATTTGGA
AGAAATAAAGCTCCCCTCAACTATTCGGAAAATAGGTGCTTTTGTCTTTCA
ATCTAATAACTTGAAATCCTTTGAAGCAAGTGAAGATTTAGAAGAGATTA
AAGAGGGAGCCTTTATGAATAATCGTATTGGAAGTCTAGACTTGAAAGAC
AACTTATCAAAATAGGTGATGCTGCTTTCCATATTAATCATATTTATGCC
ATTGTTCTTCCAGAATCTGTACAAGAAATAGGACGTTTCTGCTTTTCGACAA
AATGGTGCCTTACCTTATGTTTATCGGAAATAAGGTTAAAACAATTGGT
GAAATGGCTTTTTTATCCAATAAACTGGAAAGTGTAATCTCTCTGAGCAA
AAACAATTAAAGACAATTGAGGTCCAAGCTTTTTTCGGATAATGCCCTTAGT
GAAGTAGTCTTACCGCCAAATTTACAGACTATTCGTGAAGAGGCTTTCAA
AGGAATCATTTGAAAGAAGTGAAGGGTTCATCTACATTATCTCAGATTACT
TTAATGCTTTTGATCAAAATGATGGGGACAAACGCTTTGGTAAGAAAGTG
GTTGTTAGGACACATAATAATTCTCATATGTTAGCAGATGGTGAGCGTTTT
ATCATTGATCCAGATAAGCTATCTTCTACAATGGTAGACCTTGAAAAGGTT

FIG. 1 CONT'D

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TTAAAAATAATCGAAGGTTTAGATTACTCTACATTACGTCAGACTACTCAA
ACTCAGTTTtagagaaatgactactgcaggtaaagcgttgttatcaaaatct
AACCTCCGACAAGGAGAAAAACAAAAATTCCTTCAAGAAGCACAATTTTT
CCTTGGTCGCGTTGATTGGATAAAGCCATAGCTAAAGCTGAGAAGGCTTT
AGTGACCAAGAAGGCAACAAAGAATGGTCATTTGCTTGAGAGGAGTATTA
ACAAAGCGGTATTAGCTTATAATAATAGTGCTATTAAGCTAATGTTA
AGCGCTTGAAAAAGAGTTAGACTTGCTGACAGATTTAGTCGAGGGAAAA
GGACCATTAGCGCAAGCTACAATGGTACAAGGAGTTTATTTATTAAAGAC
GCCTTTACCATTGCCAGAATATTATATCGGATTGAACGTTTATTTTGACAA
GTCTGGAAAATTGATTTATGCACCTGATATGAGTGATACTATTGGCGAGGG
ACAAAAAGATGCATATGGTAATCCTATATTAATGTTGACGAGGATAATG
AAGGTTATCATACCTTGGCAGTTGCCACTTTAGCTGATTATGAAGGTCTTT
ATATTAAAGATATTTTAAATAGTTCCCTTGATAAGATTAAAGCAATACGCC
AGATTCCCTTGGCAAAATATCATAGATTAGGAATTTTCCAAGCTATCCGAA
ATGCAGCGGCAGAAGCAGACCGATTGCTTCCTAAGACACCTAAGGGGTAC
CTAAATGAAGTCCCAAATTATCGTAAAAACAAATGGAGAAAAATTTAA
ACCAGTTGATTATAAAACGCCGATTTTAAATAAGGCTTTACCTAATGAAAA
GGTAGACGGTGATAGAGCGGCTAAAGGTCATAATATAAATGCGGAGACTA
ATAATTCTGTAGCTGTAACACCAATAAGGTCCGAGCAGCAATTACATAAGT
CACAGTCTGATGTAAATTTACCTCAAACAAGTTCTAAAAATAATTTTATAT
ACGAGATTCTAGGATACGTTAGTTTATGTTTGCTTTTCCTAGTAAGTCTGG
GAAAAAAGGAAAACGAGCAAGAAAAATAA

MTKKHLKTLALALTTVSVVTYSQEVYGLEREESVKQEQTQSASEDDWFEEDN
ERKTNVSKENSTVDETVSDFSDGNSNNSSSKTESVSDPKQVPKAKPEVTQE
ASNSSNDASKVEVPKQDTASKKETLETSTWEAKDFVTRGDTLVGFSKSGINKL
SQTSHLVLP SHAADGTQLTQVASFAFTPDKKTAIAEYTSRLGENGKPSRLDIDQ
KEIIDEGEIFNAYQLTKLTIPNGYKSIGQDAFVDNKNIAEVNLPESLETISDYAF
AHMSLKQVKLPDNLK VIGELAFFDNQIGGKLYLPRHLIKLAERAFKSNRIQTV
EFLGSKLK VIGEASFQDNLRNVMLPDGLEKIESEFTGNPGDEHYNNQVVL R
TRTGQNP HQ LATENTYVNPDKSLWRATPDMDYTKWLEEDFTYQKNSVTGFS
NKGLQKVRRNKNLEIPKQHNGITITEIGDNAFRNVDFQSKTLRK YDLEEIKLPS
TIRKIGAF AFQSNNLKSFEASEDLEEIKEGAFMNNRIGTLDLKD KLIKIGDAAFH
INHIYAIVLPESVQEIGRSAFRQNGALHLMFIGNKVK TIGEMAFLSNKLESVNL
SEQKQLKTIEVQAFSDNALSEVVLPPNLQTIREEAFKRNHLKEVKGSSTLSQITF
NAFDQNDGDKRFGKKVVVRTHNNSHMLADGERFIIDPKLSSTMVDLEKVL
KIEGLDYSTLRQTTQTQFREMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGR
VDLDKAIKAEKALVTKKATKNHLLERSINKAVLAYNNSAIKKANVKRLEK
ELDLLTDLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA
LDMSDTIGEGQKDAYGNPILNVDEDNEGHTLAVATLADYEGLYIKDILNSSL
DKIKAIRQIPLAKYHRLGIFQAIRNAAAEADRLLPKTPKGYLNEVPNYRKKQM
EKNLKPVDYKTIPIFNKALPNEKVDGDRAAKGHNINAETNNSVAVTPIRSEQQL
HKSQSDVNL PQTSSKNFIYEILGYVSLCLLFLVTAGKKGKRARK*

FIG. 1 CONT'D

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Sequence description:

- A] Length 3168 bp - 1056 aa (Partial sequence)
B] Obvious signal peptide with Shine Dalgarno
sequence upstream of the ATG start codon.

ID-88

Clone RS-56

GCAGGATACATCATGCACAAGCACGAGGCTATCGTGTCATGCTGGGGTCA
ACCCAGGAAGACATGTCGGCACAAGCTGAAGATTTCTTTACAGTCTGTACA
CAATAAAGAGACGGGTAAGAGCGCTTTTAATGACAAAGAACGACTAGCAA
TT

AGYIMHKHEAIVSCWGQPRKTCRHLKISLQSVHNKETGKSAFNDKERLAI

Sequence description:

- A] Length:153 bp - 51 aa (partial sequence)
B] No signal peptide visible, insufficient
sequence data to determine the presence of a
Shine Dalgarno sequence.

ID-89

Clone RS-58

GTGTCATTTATGCAAAGAAAATCCTATTTAAAATCCATGAGTGTTCTTACT
TTAACAGCTTGTCTTATATCAGGATATGTGGTTAAAGATATTGCTATGTTA
CATGCAGTATCTGCCAGTGAGAAGAAAGCAAATAATGTCAGTCCGAGAGA
AAATCTCTACAGGGCTGTCAATGATAATTGGCTAGCCAATACAAAACCTCA
AACAAGGGCAGACTAGTGTTAATAGTTTTTCAGAAATTGAGGATAAATTA
AAGCAACTGTTAGTGTCTGATATGGCTAAAATGGCCTCAGGAAAGATTGA

FIG. 1_{CONT'D}

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AACAACCAATGATGAACAGAAAAAATGGTTGCATACTATAAACAAGGTA
TGGACTTTAAAAACAAGAGATAAAAAATGGTCTCAAACCTCTAAAACAGTT
TTACAAAAACTTGAAGCAGTCTCTTCAATGAAAGACTTTCAAAGTTTGGCC
CATGATTTTGTGATGAGTGGTTTTGTTTTACCATTTGGTTTGACTGTGGAAA
CCAATGCTCGAGATAATAGCCAAAAGCAATTGGTGCTTCGTCAAGCACCC
GCATTACTTGAATCACCTGACCAATATAAGAAGGGCAATAAAGAAGGTGA
GGCTAAATTATCAGCTTACCGTACTTCAGCAATGGCTTTGCTTAAACAAGC
TGAAAAAGTAACATTGAAGATAGAAAAGTAAACAAGCTATAGCAT
TTGATAGACTCTTATCAGAAAAAACGCAAGTTGATCAAAGTAAATCACA
GCTGAAAGTGAGACAGCTGCGGGGCGATATAACCCTGAAAGTATGGAAAC
GGTTCACAATTACGCCAAGGAATTTGACTTTAAAGAATTGATTGAAAAACT
AGTTGGGCCAACGAATAAGGCAGTCAATGTAGAAGATAAAACTTATTTTA
AACAGGTAAATGATGTTATAAATAGTAAACAATTAGCCAATATGAAAGCA
TGGATGATGATTTCTATGCTAGTTGATCAATCAGATTTTCTAGGAGAACAA
AATCGTCAAGCAGCGAGTGCTTTTAAGAATGTTGCGTCTGGTTTGACTCAG
ATTGAATCGAAAGAAAAAATGCTTACACCCAATTAG

MSFMQRKSYLKSM SVLT LTACLISGYVVKDIAM LHAVSASEKKANNVSPREN
LYRAVNDNWLANTKLKQGQTSVNSFSEIEDKLKQLLVSDMAKMASGKIETTN
DEQKKMVA YYKQGMDFKTRDKNGLKPLKPV LQKLEAVSSMKDFQSLAHDF
VMSGFVLPFGLTVETNARDNSQKQLVLRQAPALLES PDQYKKG NKEGEAKLS
AYRTSAMALLKQAGKSNIEDRKL VKQAIAFDRL LSEKTQVDQSKITAESETAA
GRYNPESMETVHNYAKEFD FKELIEKL VGPTNKAVNVEDKTYFKQVNDVINS
KQLANMKAWMMISMLVDQSDFLGEQNRQAASAFKNVASGLTQIESKEKMLT
PN*

Sequence description:

- A] Length: 1095 bp - 365 aa (full length gene)
- B] an GTG (possible ATG start codon located 7 bp further downstream) start codon with an obvious signal peptide. Shine Dalgarno sequence present upstream of the ORF.

ID-90

Clone RS-59

FIG. 1_{CONT'D}

15 / 110

ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTTAAATGAG
TATTGATAAACTTAGATATAAAGAACCAGAGAGTGAACATGACAAGCGAC
CTACTTTTTATTTGGTAGTACTTATACTTGTTACTGTAGCAGTTATATTGTC
GTTATTTAAATATTTTTTATAG

MEMPKRNELLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTAVILSLFK
YFL*

Sequence description:

- A) Length: 174 bp - 58 aa(full length gene)
- B) No obvious signal peptide, but Shine
Dalgarno sequence is present upstream of ATG
start codon.

ID-91

Clone RS-62 (partial sequence)

ATGCAGGTATTTTTAAATATTGTCAATAAATTCTTTGATCCAGTTATTCATA
TGGGTTCGGGAGTTGTGATGCTAATTGTCATGACAGGTTTAGCCATGATAT
TTGGAGTGAAGTTTTCTAAAGCACTTGAAGGTGGTAT

MQVFLNIVNKFFDPVIHMGSGVVMLIVMTGLAMIFGVKFSKALEGG

Sequence description:

- A) Length: 141 bp - 41 aa (partial sequence)
- B) Shine Dalgarno sequence present upstream of
ATG start codon with a possible signal peptide
present

ID-92

FIG. 1 CONT'D

16 / 110

Clone RS-69 (partial sequence)

ATGAAAAAGAAAACATTCAGTGCTTATAACTTTTTAACGGCTCTTATCCTT
TGTCCTTTTGACAGTGCTTTTTATCTTTCCATTTTATTGGATTATGACAGGAG
CTTTTAA

MKKKTFSAYNFLTALILCLLTVLFIFPFYWIMTGAF

Sequence description:

- A) Length: 110 bp -36 aa (Partial sequence)
B) Possible signal peptide with Shine Dalgarno
sequence directly upstream of the ATG start
codon.

ID-93

Clone RS-70

ATGACTGAGAACTGGTTACATACTAAAGATGGTTCAGATATTTATTATCGT
GTCGTTGGTCAAGGTCAACCGATTGTTTTTTTACATGGCAATAGCTTAAGT
AGTCGCTATTTTGATAAGCAAATAGCATATTTTTCTAAGTATTACCAAGTT
ATTGTTATGGATAGTAGAGGGCATGGCAAAAGTCATGCAAAGCTAAATAC
CATTAGTTTCAGGCAAATAGCAGTTGACTTAAAGGATATCTTAGTTTCATTT
AGAGATTGATAAAGTTATATTGGTAGGCCATAGCGATGGTGCTAATTTAGC
TTAGTTTTTTCAAACGATGTTTCCAGATATGGTTAGAGGGCTTTTGCTTAAT
TCAGGGAACCTGACTATTCATGGTCAGCGATGGTGGGATATTCTTTTAGTA
AGGATTGCCTATAAATTCCTTCACTATTTAGGGAAACTCTTCCGTATATG
AGGCAAAAAGCTCAAGTTATTTTCGCTTATGTTGGAGGATTTGAAGATTAGT
CCAGCTGATTTACAGCATGTGTCAACTCCTGTAATGGTTTTGGTTGGAAAT
AAGGACATAATTAAGTTAAATCATTCTAAGAACTTGCTTCTTATTTTCCA
AGGGGGGAGTTTTATTCTTTAGTTGGCTTTGGGCATCACATTATTAAGCAA
GATTCCCATGTTTTTAATATTATTGCAAAAAGTTTATCAACGATACGTTG
AAAGGAGAAATTGTTGAAAAAGCTAATTGA

MTENWLHTKDGSDIYYRVVGQQPIVFLHGNSLSSRYFDKQIAYFSKYYQVIV
MDSRGHGKSHAKLNTISFRQIAVDLKDILVHLEIDKVILVGHSDGANLALVFQ

FIG. 1_{CONT'D}

17 / 110

TMFPDMVRGLLLNSGNLTIHGQRWWDILLVRIAYKFLHYLGKLFYPYMRQKA
QVISLMLEDLKISPADLQHVSTPVMVLVGNKDIIKLNHKKLASYPFRGEFYSL
VGFGHHIIKQDSHVFNIIAKKFINDTLKGEIVEKAN*

Sequence description:

- A] Length: 744 bp - 248 aa (full length gene)
- B] No obvious signal peptide, but Shine
Dalgarno sequence upstream of the ATG start
codon.

ID-94

Clone RS-71

ATGGTAGCAAAAGAGTTAGGTAAAAATAGCTTTACTATCCCAACTATTTGT
TCTAATTGCTCCGCAGGTACTGCCATTGCAGTTGTATATAATGATGACCAT
TCTTTCTTAAGATACGGCTATCCCGAGTCTCCACTTCATATTTTATCAATA
CACGGATCATTGCACAGGCACCAAGCAAATATTTTGGGCTGGTATTGGGG
ACGGTATTTCAAAGCCCCCTGAAGTAGAACGTGCTACCTTAGAGGCTAAG
ACCAATAAACTACCACATACTGCAGTGTTAGGACAAGCAGTCGCTCTGTCT
TCAAAGGAAGCTTTTATCAATTTGGTGAACAAGGTCTAAAAGACGTTGAA
GCTAATTTAGCTTCGCGTGCAGTTGAAGAAATTGCGCTTGATATCTTA

MVAKELGKNSFTIPTICSNCSAGTAIAVVYNDHDSFLRYGYPE SPLHIFINTRIIA
QAPSKYFWAGIGDGISKAPEVERATLEAKTNKLPHTAVLGQAVALLSKEAFY
QFGEQGLKDVEANLASRAVEEIALDIL

Sequence description:

- A] Length: 405 bp - 135 aa (Partial sequence)
- B] No obvious Shine Dalgarno sequence upstream
of the ATG start codon, probable signal
peptide present at the N-terminus.

ID-95

FIG. 1 CONT'D

18 / 110

Clone RS-73

TTGAGGGAAACTTACTGGAAAATTTCAAGCGATTGCGATAAAAATAAATCCTT
GCAGAGTTTTCTAGAGAAAGGAGGTCAGATTTATTGGAGTGGCAAGATCT
AGCGCAGTTACCTGTATCTATTTTTAAAGACTATGTTACAGATGCTCAAGA
CGCGGAAAAACCTTTTATATGGACAGAAGTATTTTAAAGGGAGATTAATCG
CTCAAATCAAGAAATTATTTTGCATATTTGGCCGATGACTAAGACAGTCAT
TCTGGGGATGTTAGATCGAGAATTACCACATTTAGAATTAGCTAAAAAAG
AAATCATCAGTCGTGGTTATGAACCAGTTGTTCCGAATTTTGGAGGTCTCG
CAGTTGTAGCTGATGAAGGAATTTTAAATTTTTCATTGGTTATTCCAGATGT
TTTTGAGAGAAAATTGTCTATCTCAGATGGGTATCTTATAATGGTCGATTTT
ATTAGAAGTATATTTTCGGATTTTTATCAACCTATTGAGCACTTTGAAGTA
GAGACCTCCTATTGTCCTGGTAAGTTTGATCTTAGTATAAATGGCAAAAAA
TTTGCTGGCTTGGCTCAGCGCCGTATAAAGAATGGTATTCCGGTATCAATT
TACCTTAGCGTTTGTGGCGATCAAAAAGGGCGGAGTCAAATGATTTTCAGAT
TTTTATAAGATTGGTCTAGGTGATACGGGTAGTCCAATTGCTTATCCAAAT
GTAGATCCTGAAATTATGGCTAATCTATCTGATCTATTAGATTGTCCTATG
ACAGTAGAAGATGTTATTGATCGTATGTTGATTAGCCTTAAACAAGTAGGT
TTTAATGATCGTTTACTGATGATTAGACCCGATTTAGTTGCAGAGTTTGAT
AGATTTTCAGGCTAAGTCTATGGCTAATAAGGGGATGGTGAGCAGAGATGA
ATAA

MRETYWKISSDCDKINLAEFSRERRSDLLEWQDLAQLPVSIFKDYVTDAQDAE
KPFIWTEVFLREINRSNQEILHIWPMTKTVILGMLDRELPHLELAKKEIISRGYE
PVVRNFGGLAVVADEGILNFSLVIPDVFERKLSISDGYLIMVDFIRSIFSDFYQPI
EHFEVETSYCPGKFDLSINGKKFAGLAQRRIKNGIAVSIYLSVCGDQKGRSQMI
SDFYKIGLGDGTGSP IAYPNVDPEIMANLSDLLDCPMTVEDVIDRMLISLKQVGF
NDRLLMIRPDLVAEFD RFQAKSMANKGMVSRDE*

Sequence description:

- A] Length: 921 bp -307 aa (Full-length gene sequence)
- B] No obvious Shine Dalgarno sequence upstream
of the TTG start codon or signal peptide
visible. Actual start point may be a further
85 bp downstream (TTG). This start point is
preceded by a typical Shine-Dalgarno sequence.

FIG. 1 CONT'D

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ID-96

Clone RS-74

TTGGAAGGTTTACTTATTGCATTGATTCCCATGTTTGCGTGGGAAAAGTATT
GGATTTGTTAGTAATAAAAATTGGAGGGCGTCCAAATCAACAAACATTTGG
AATGACTTTAGGAGCATTGCTATTTGCGATTATCGTATGGTTATTTAAACA
GCCAGAGATGACTGCCTCATTGTGGATTTTGGTATCTTAGGTGGTATCCT
ATGGTCAGTCGGCCAAAATGGTCAATTTCAAGCAATGAAATATATGGGAG
TCTCTGTTGCTAATCCACTGTCAAGTGGTGCACAATTAGTAGGTGGAAGCC
TAGTTGGTGCTTTAGTCTTTTCATGAATGGACTAAGCCAATCCAATTTATTTT
AGGATTGACAGCGTTGACATTATTAGTTATCGGCTTCTATTTCTCAAGTAA
ACGTGATGTTTCAGAACAAGCTTTGGCAACACATCAAGAGTTTTCAAAAG
GATTTGCTACAATTGCTTATTCAACTGTAGGTACATCTCGTACGCAGTTTT
ATTTAACAACATTATGAAGTTCGACGCTATGGCCGTCATTTTACCCATGGC
TGTTGGAATGTGTCTAGGTGCAATTTGTTTCATGAAGTTTCGTGTAACTTT
GAGGCTGTTGTTGTTAAAAATATGATTACAGGTCTCATGTGGGGCGTTGGT
AATGTCTTCATGTTATTGGCAGCAGCTAAAGCAGGGCTAGCAATTGCTTTT
AGTTTTTCTCAACTTGGAGTAATTATCTCTATTATTGGTGGTATTTTATTTT
AGGTGAGACAAAAACGAAGAAAGAGCAGAAATGGGTGTCATGGGTATC
CTTTGTTTTGTTATGGGTGCTATATTACTTGGTATTGTTAAATCTTATTAA

MEGLLIALIPMAWESIGFVSNKIGGRPNQQTFGMTLGALLFAIIVWLFKQPEM
TASLWIFGILGGILWSVGQNGQFQAMKYMGVSVANPLSSGAQLVGGSLVGAL
VFHEWTKPIQFILGLTALTLLVIGFYFSSKRDVSEQALATHQEFSKGFATIAYST
VGYISYAVLFNNIMKFDAMAVILPMAVGMCLGAICFMKFRVNFEAVVVKNMI
TGLMWGVGNVFMLLAAAKAGLAIASFSQLGVIISIIGGILFLGETKTKKEQK
WVVMGILCFVMGAILLGIVKSY*

Sequence description:

- A] Length: 867 bp - 289 aa (full-length gene)
- B] Possible Shine Dalgarno sequence upstream of
GTG start codon, no obvious signal peptide
present.

ID-97

FIG. 1_{CONT'D}

20 / 110

Clone RS-75

ATGACAACCTTACTACGAAGCTATAAACTGGAACGAAATTGAAGATGTTAT
TGATAAATCAACTTGGGAAAACTAACCGAACAATTTTGGCTCGATACAC
GTA^TCCCTTTATCAAATGACTTAGACGATTGGCGCAAAC^TTTCCGCTCAAG
AAAAAGATCTTGTTGGCAAGGTTTTTGGAGGCTTAACCCTACTTGATACCA
TGCAATCAGAACTGGTGTGAAGCTATTCGTGCCGATGTTCGCACGCCTC
ACGAAGAAGCTGTCTTAAACAATATTCAATTCATGGAATCTGTTACGCTA
AATCTTATTCTTCAATTTTCTCAACTTTAAATACTAAATCAGAAATTGAAG
AAATTTTCGAGTGGACTAATAATAATGAGTTCCTTCAAGAAAAAGCACGT
ATTATCAATGACATTTATGCTAATGGAAATGCCCTTCAAAAAAAGGTGGCT
TCCACCTACCTCGAAACTTTCCTTTTTTATTCTGGCTTTTTTACACCTCTTTA
CTATTTGGGAAATAATAAGTTAGCAAATGTTGCTGAAATCATTAAATTAAT
TATTCGTGATGAATCTGTACATGGTACTTATATCGGTTACAAATCCAGCTT
GGTTTTAACGAATTACCAGAAGATGAGCAAGAGAATTTTCGTGATTGGAT
GTATGACCTCCTTTATCAGCTGTATGAAAACGAAGAAAAATACACCAAGA
CACTTTATGATGGCGTAGGATGGACTGAAGAAGTTATGACCTTTTTACGCT
ACAATGCTAATAAAGCTCTTATGAATTTAGGACAAGATCCTTTATTCCCAG
ATACAGCAAATGATGTCAACCCAATTGTTATGAATGGTATTTCAACAGGAA
CATCAAACCATGACTTCTTCTCTCAAGTAGGTAATGGTTACCTACTTGGTA
GCGTTGAAGCTATGCATGATGACTATAACTATGGATTATAA

MTTYYEAINWNEIEDVIDKSTWEKLTEQFWLDTRIPLSNDLDDWRKLSAQEK
DLVGKVFGGLTLLDTMQSETGVEAIRADV RTPHEEAVLNNIQFMESVHAKSY
SSIFSTLNTKSEIEEIFEWTNNNEFLQEKARIINDIYANGNALQKKVASTYLETF
LFYSGFFTPLYLGNKLANVAEIIKLIIRDES VHGTYIGYKFQLGFNELPEDEQ
ENFRDWMYDLLYQLYENEEKYTKTLYDGVGWTEEVMTFLRYNANKALMNL
GQDPLFPDTANDVNPVMNGISTGTSNHDFFSQVGNGYLLGSVEAMHDDDDYN
YGL*

Sequence description:

- A) Length: 960 bp - 320 aa (full length gene)
- B) Shine Dalgarno sequence present upstream of
ATG start codon, but no signal peptide
present.

ID-98

FIG. 1^{CONT'D}

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Clone RS-77 (partial sequence)

ATGAATTGGTCACGTATCTGGGAACCTCGTAAAAATTAATATCCTTTATTCA
AACCCCTCAGACTCTATCGGCACTAAGAAAAAAGCAAGAAAAGCATCCTAA
AAAAGAATTTTCAGCTTATAAATCCATGTTTAGAAATCAGTTATTTTCAGAT
TTTGCTCTTTTCAATAATTTATGTATTTCTCTTTGTATCACTTGATTTTAAAG
AATATCCGGGCTATTTACGTTCTACATTGGTATCTTTACACTAGTATCCAT
TATCTACTCTTTTATTGCGATGTACAGTGTTTCTATGAGAGTGACGATGTT
AA

MNWSRIWELVKINILYSNPQTLALRKKQEKHPKKEFSAYKSMFRNQFLQILL
FSIIYVFLFVSLDFKEYPGYFTFYIGFTLVSIISFIAMYSVFYESDDV

Sequence description:

- A] Length: 311 bp - 103 aa (Partial sequence)
- B] Shine Dalgarno sequence present upstream of
ATG start codon, no obvious signal peptide at
N-terminus.

ID-99

Clone RS-78 (partial sequence)

TAATCTTTTAGTCAACGGAGCAACAGGAAAATTGCAGGCTATGCGACAGA
TATTCCACCACATAATTTAGCAGAAGTCATTGATGCTGTCGTGTACATGAT
TGATCACCTAAAGCTAAATTAGATAAATTAATGGAATTTCTACCTGGTCC
AGATTTTCCAACCTGGCGCTATCATTCAAGGAAAAGATGAAATTCGTAAGG
CATATGAGACTGGTAAGGGGAGAGTAGCGGTTTCGCTCGCGAACTGCTATT
GAAACCTTAAAAGGTGGTAAGAAACAAATTATTGTTACTGAAATTCCTTAT
GAAGTTAAT

SFSQRSNRKIAGYATDIPPHNLAEVIDAVVYMIDHPKAKLTKLMEFLPGPDFPT
GAIQGGKDEIRKAYETGKGRVAVRSRTAIETLKGGKKQIIVTEIPYEVN

Sequence description:

- A] Length: 312 bp - 104 aa (Partial sequence)
- B] No obvious Shine Dalgarno sequence or a

FIG. 1 CONT'D

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signal peptide. Both N- and C- termini of ORF
yet to be elucidated.

ID-100

Clone RS-79

ATGGGACGTAAGTGGGCCAATATTGTTGCCAAAAAGACTGCTAAAGATGG
TGCTAACTCAAAAGTATACGCTAAATTCGGTGTGAAATATATGTTGCTGC
AAAGCAAGGTGAACCAGACCCCGAGTCAAACCTCAGCTCTAAAATTCGTTT
TGGACCGTGCTAAGCAAGCACAAAGTTCCAAAGCATGTTATTGATAAAGCG
ATTGATAAAGCCAAAGGAAACACAGATGAAACTTTTCGTAGAGGGACGCTA
TGAAGGTTTTGGTCCAAATGGTTCAATGATTATTGTGGATACTTTGACATC
AAATGTTAACCGTACGGCAGCAAATGTACGTAAGTCTTACGGTAAGAACG
GTGGCAATATGGGAGCTTCAGGATCGGTATCCTACTTATTTGATAAAAAAG
GTGTCATCGTTTTTGGTGGTATGATGCTGACACTGTCTTCGAACAATTACT
TGAAGCGGATGTAGACGTAGATGATGTTGAAGCAGAAGAGGGAACAATA
ACAGTTTATACCGCCCCAACAGATCTTCATAAAGGTATCCAAGCACTTCGC
GATAATGGTGTAGAAGAATTCCAAGTACTGAACTTGAAATGATTCCTCAA
TCAGAAGTAGTATTGGAAGGTGATGACCTTGAACTTTTGAAAAGCTT

MGRKWANIVAKKTAKDGANSKVYAKFGVEIYVAAKQGEPPESNSALKFVL
DRAKQAQVPKHVIDKAIDKAKGNTDETFVEGRYEGFGPNGSMIIVDTLTSNV
NRTAANVRTAYGKNGGNMGASGSVSYLFDKKGVIVFAGDDADTVFEQLLEA
DVDVDDVEAEEGTITVYTAPDLHKGIALRDNGVEEFQVTELEMIPQSEVVL
EGDDLETFEKL

Sequence description:

- A] Length: 654 bp - 218 aa (Partial sequence)
- B] Possible Shine Dalgarno sequence upstream
of ATG start, no obvious signal peptide

ID-101

Clone RS-80

FIG. 1 CONT'D

23 / 110

TTGGAGAAATATTTGAAGAACCCGATTACATGGATTGGATTAGTTCTTGTG
GTTACGTGGTTTTTAATACTAAAAGTAGTGAATTTTGGTGTGTGTG
TCTTGTGTAGTATTTGCTAGTCAAAGTGAT

MEKYLKNPITWIGLVLVVTWFLTKSSEFLIFGVCVLLLVFASQSD

Sequence description:

- A] Length: 135 bp - 45 aa (partial sequence)
- B] Shine Dalgarno sequence upstream of TTG start codon with possible signal peptide evident at N-terminus.

ID-102

Clone RS-81

ATGACACAATCAGATGCATATCTCTCGTTGAACGCGAAGACACGCTTTAGA
GATCGCACAGGTAATTATCATTTTACTTCGGATAAAGAGGCTGTTGAACAA
TATATGATAGAACATGTTGAACCTAATACGATGGTGTTCACATCACTAATT
GAAAAGCTAGATTATTTGGTTTCTAATAACTACTATGAATCGGACCTTCTA
AAACAATATAACCTTGAGTTTATTTGCCAAATTTTGGAGCATGCATACGCT
AAGAAATTTGCTTTTCTAAATTTTATGGGGGCTTTAAAATTTTATAATGCTT
ATGCTCTTAAT

MTQSDAYLSLNAKTRFRDRTGNYHFTSDKEAVEQYMIEHVEPNTMVFTSLIE
KLDYLVSNYYESDLLKQYNLEFICQIFEHAYAKKFAFLNFMGALKFYNAYA
LN

Sequence description:

- A] Length: 318 bp - 106 aa (Partial sequence)
- B] Shine Dalgarno sequence present upstream of ATG start codon, no obvious signal peptide

FIG. 1 CONT'D

24 / 110

ID-103

Clone 2-11A

ATGGTATTTATGGCAAATAAGAAAAAACAAGGAAAGAAAACCAGAA
GACCTACTAAGGCAGAAATAGAGCGTCAAAGAGCTATTCAAAGGATGATT
ACTGCTCTTGTTTTAACAATTATTCTCTTTGGTATTATCAGATTAGGTA
TTTTTGGTATTACAGTCTATAACGTCATCCGTTTTATGGTAGGTAGCTTGGC
TTACTTATTTATTGCGGCAACTTTAATCTACCTTTATTTCTTTAAATGGTTG
CGAAAGAAAGATAGCTTAGTAGCAGGTTTTTGATAGCTTCTTTAGGATTA
TTGATTGAGTGGCATGCTTACCTTTTCTCAATGCCTATTTTGAAAGATAAA
GAAATTTTTCGTTCAACTGCTCGATTAATTGTGTCTGATTAAATGCAATTTA
AAATCACTGTTTTTGCCGGTGGAGGTATGTTGGGTGCTTTGATTTACAAGC
CAATTGCTTTTCTCTTTTCTAATATTGGTGCCTATATGATTGGTGTTCTCTTC
ATCATTTTGGGTCTCTTTTAATGAGTTCTCTGGAAGTTTATGACATCGTCG
AATTTATTAGAGCTTTTAAAAATAAAGTGGCAGAGAAGCACGAGCAAAAT
AAAAAGGAGCGTTTTGCTAAGCGAGAGATGAAAAAGCAATCGCTGAACA
AGAGCGCATAGAGCGTCAAAAAGCTGAAGAAGAAGCTTATTTAGCTTCGG
TTAATGTAGACCCTGAAACGGGTGAGATTCTAGAGGATCAAGCTGAGGAC
AATTTGGATGATGCGCTACCACCTGAGGTAAGTGAAACATCAACTCCGGT
ATTTGAGCCAGAGATCCTTGCTTATGAGACATCGCCTCAAAATGATCCTTT
ACCAGTAGAGCCGACAATTTATTTAGAAGACTATGATTCGCCGATTCTTAA
TATGAGAGAAAATGATGAGGAAATGGTTTATGATTTAGATGATGATGTAG
ATGATAGTGATATAGAAAATGTCGACTTTACACCTAAAACGACACTGGTTT
ATAAATTACCAACGATAGATTTATTTGCACCAGATAAGCCTAAAAATCAAT
CCAAAGAAAAGGATTTAGTCCGAAAGAATATCAGAGTTTTAGAAGAAACA
TTTAGAAGTTTTGGTATCGATGTAAAAGTAGAACGTGCTGAAATTGGACCA
TCAGTTACTAAATATGAAATTAAACCAGCAGTTGGAGTTCGTGTGAATCGT
ATTTCAAATCTATCTGACGACCTAGCTCTTGCTCTTGACAGCAAAAGATGTG
CGTATAGAAGCACCAATTCCTGGAAAATCATTAAATAGGTATTGAAGTTCCT
AACTCAGAAATTGCAACGGTTTCTTTCCGCGAAGTTTGGGAACAATCTGAT
GCCAATCCTGAAAACCTTTTAGAAGTACCACTAGGAAAAGCTGTAAACGG
CAATGCTCGCAGTTTTAACTTAGCTAGAATGCCGCATCTTTTGGTAGCTGG
TTCAACTGGTTCAGGTAAATCTGTGGCAGTTAATGGAATTATTTCAAGTAT
TTTGATGAAGGCACGTCCAGATCAAGTTAAGTTTATGATGATTGATCCCAA
AATGGTTGAATTATCTGTTTATAATGATATTCCACATTTATTAATCCCTGTT
GTAACCAATCCGCGTAAAGCAAGTAAGGCACTCCAAAAAGTTGTTGATGA
AATGGAAAATCGATACGAGTTATTTAGCAAAATTGGTGTGCGTAATATAG
CAGGTTATAATACAAAGGTTGAAGAGTTTAAATGCTTCCTCTGAGCAAAAAC
AAATGCCTTTGCCTTTAATCGTTGTCAATTGTAGATGAATTGGCTGACTTGAT
GATGGTTGCTAGTAAAGAAGTTGAAGATGCTATTATTCGTTTGGGGCAAAA
AGCACGTGCTGCAGGTATCCATATGATTCTTGCAACTCAACGTCCATCCGT

FIG. 1_{CONT'D}

25 / 110

AGATGTTATTTCTGGTTTGATTAAAGCAAATGTTCCGTCGCGTATTGCATTT
 GCTGTTTCAAGTGGTACTGATAGCCGTACGATCCTTGATGAAAATGGTGCT
 GAAAAGCTCTTGGGACGGGGTGACATGCTCTTTAAGCCTATTGATGAGAAT
 CATCCAGTACGACTACAAGGTTCTTTATTTTCAGATGATGATGTTGAAAGG
 ATCGTTGGTTTTATCAAAGACCAAGCCGAGGCTGACTATGATGATGCCTTT
 GATCCTGGAGAAGTATCTGAAACAGATAACGGCTCTGGTGGTGGCGGCGG
 AGTACCTGAAAGTGATCCTCTTTTTGAAGAAGCCAAGGGACTCGTTTTAGA
 GACGCAAAAAGCAAGTGCCTCAATGATTCAACGCCGATTGTCTGTTGGTTT
 CAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCGGGGGTTATTG
 GTCCAGCAGAAGGAACCAAGCCACGAAAAGTTTTAATGACTCCAACCTCCG
 AGTGAATAA

MVFMANKKKTKGKKTRRPTKAEIERQRAIQRMITALVLTIIFFGIIRLGIFGIT
 VYNVIRFMVGLAYLFIAATLIYLYFFKWLRKKDSL VAGFLIASLGLLIEWHA
 YLFSMPILKDKEILRSTARLIVSDLMQFKITVFAGGGMLGALIYKPIAFLFSNIG
 AYMIGVLFILGLFLMSSLEVYDIVEFIRAFKNKVAEKHEQNKKERFAKREMK
 KAIAEQERIERQKAEIEEAYLASVNVDPETGEILEDQAEDNLDDALPEVSETST
 PVFEPEILAYETSPONDPLPVEPTIYLEDYDSPINMRENDEEMVYDLDDVD
 SDIENVDFTPKTTLVYKLPTIDLFAPDKPKNQSKEKDLVRKNIRVLEETFRSFGI
 DVKVERAEIGPSVTKYEIKPAVGVRVNRISNLSDDLALALAAKDVRIEAPIGK
 SLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLARMPH
 LLVAGSTGSGKSVAVNGHISSILMKARPDQVKFMMIDPKMVELSVYNDIPHLLI
 PVVTNPRKASKALQKVDEMENRYELFSKIGVRNIAGYNTKVEEFNASSEKQ
 QMPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVD
 VISGLIKANVPSRIAFVSSGTDSTRITLDENGAEKLLGRGDMLFKPIDENHPVRL
 QGSFISDDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGSGGGGGVPESDPL
 FEEAKGLVLETQKASASMIQRRLSVGFNRATRLMEELEAAGVIGPAEGTKPRK
 VLMTPTPSE*

Sequence description:

- A) Length: 2451 bp - 817 aa (Full-length gene)
- B) Shine Dalgarno sequence present upstream of
ATG start codon, possesses a potential signal
peptide

ID-104

Clone 2-18/22b

FIG. 1^{CONT'D}

26 / 110

ATGTCACAAGAGCAAGGAAAAATTTATATTGTAGAAGATGATATGACGAT
TGTGTCACTTTTAAAAGATCATTTATCAGCTAGCTATCATGTCTCTAGTGTC
AGCAATTTTCGTGATGTGAAACAAGAAATTATCGCATTTC AACCCGATTTG
ATACTAATGGATATTACGTTACCCTATTTAATGGTTTTTACTGGACTGCAG
AATTGCGTAAGTTTTTAACAATTCCTATTATTTTCATTTTCATCTAGTAATGA
TGAAATGGATATGGTTATGGCATTAAATATGGGGGGTGATGACTTTATTTT
AAAACCATTTCTCTCTAGCTGTATTAGATGCTAAGCTAACTGCTATTTTAAG
GAGAAGTCAACAATTTATCCAACAGGAATTAAC TTTGGGGGATTTACGTT
GACAAGAGAAGGGTTATTGTCTAGCCAAGATAAAGAGGGTTATTTTATCGC
CAACAGAAAATAAAATCCTATCTATCTTGCTCATGCATCCTAAACAAGTAG
TCTCAAAAAGAGTCTCTATTAGAGAACTTTGGGAAAATGATAGTTTTATTG
ATCAAAATACACTTAATGTTAATATGACACGCTTACGTAAAAAAATTGTCC
CAATAGGTTTTGATTACATTCATACAGTGAGAGGAGTTGGGTATTTACTAC
AATGA

MSQEQGKIYIVEDDMTIVSLLKDHLASASYHVSSVSNFRDVKQEIIAFQPDILM
DITLPYFNGFYWTAELRKFLTPIIFISSNDEMMDVMALNMGGDDFISKPFSLA
VLDAKLTAILRRSQQFIQQLTFGGFTLTREGLLSSQDKEVILSP TENKILSILLM
HPKQVVSKESSLLEKLWENDSFIDQNTLVNVMTRLRKKIVPIGFDYIHTVRGVG
YLLQ*

Sequence description:

A) Length: 669 bp - 223 aa (full-length gene
sequence)

B) Shine Dalgarno sequence present upstream of a GTG start codon.
Was not identified directly by LEEP. This gene was found upstream of
gene ID-10 described in WO 00/06736.

ID-105

Clone 2-20

ATGTATCAAACCTCAGACAAATAAGGAAAAATTTGTTTTATTTTTGAAATTA
TTTATCCCAGTATTGATTTATCAATTTGCTAATTTTTCAGCTACTTTTATTGA
TTCGGTTATGACTGGACAGTATAGTCAGCTACATTTGGCAGGTGTGTCAAC
TGCTAGTAATTTATGGACTCCGTTTTTCGCTTTATTAGTAGGTATGATTTCA
GCATTAGTACCAGTAGTTGGTCAACATTTGGGTAGAGGAAATAAAGAACA
AATTCGCACAGAATTTTCATCAATTTCTATATTTAGGTTTGATACTGTCCTTA
ATATTATTTTAAATCATGCAATTTATTGCTCAACCTGTCTTGGGGAGTTTGG

FIG. 1_{CONT'D}

27 / 110

GTTTAGAAGATGAAGTTCTAGCAGTTGGTCGTGGTTATTTAAATTATATGT
TGATTGGAATCATGCCGCTGGTGTGTTTAGCATTTGCCGTTTCATTCTTTGA
TGCATTGGGGTTAACAAGGTTATCTATGTATCTGATGCTTTTAATTCTACCC
TTTAATTCATTTTTTAATTATATGCTTATCTACGGTAAATTTGGTATGCCTA
GACTAGGAGGTGCGGGGGCAGGTCTTGGAACCTCTTTAACTTATTGGGCTA
TTTTTATTGGTATTATTATTGTGATGTCACTTCATCCTCAAATTAACATA
TCATATATGGACTCTGGAAAGAATAAAAGCTCCTTTGATTATTGAAGATAT
TCGATTGGGATTACCGATTGGTTTACAAATTTTGCAGAAGTTGCAATTTTT
GCAGTAGTAGGCTTATTCATGGCAAAATTTCTTCAATCATTATTGCAGCA
CATCAGGCTGCTATGAATTTTTCATCATTAAATGTATGCATTTCCTTAAGTA
TTTCCACTGCTCTAGCTATTACAATATCGTTTGAAGTAGGGGCAGAGCGCT
TTCAGGACGCAACCACTTATAGTAGGATAGGACGCTTAACAGCGGTAGGG
ATTACATCAGGAACCTTACTATTTTTATTTCTATTTTCGTGAGAATGTAGCAG
CAATGTATAATAGTGCCCTCACTTTGTGCGCTATTACAGCTCAATTCCTAAC
TTATAGTCTCTTTTTCCAGTTTGCAGATGCTTATGCAGCTCCTGTACAGGGG
ATTTTACGAGGCTATAAGGATACAACAAAACCATTTATGATCGGTGCGGG
CTCTTATTGGTTATGTGCTTTGCCATTAGCGGTTATCTTAGAAAAAATAG
CCAGTTAGGTCCGTTTGCCTATTGGATTGGTTAATCACAGGTATTTTTGTT
TGTGGTCTATTTCTAAACCAACGTCTGCAAAAGATTAAGAAGTTGTATTAT
TAA

MYQTQTNKEKFVLFKLFLIPVLIYQFANFSATFIDSVMTGQYSQLHLAGVSTAS
NLWTPFFALLVGMISALVPVVGQHLGRGNKEQIRTEFHQFLYLGLLSLILFLI
MQFIAQPVLGSLGLEDEVLA VGRGYLNYMLIGIMPLVLFSSICRSFFDALGLTRL
SMYLMLLILPFNSFFNYMLIYGKFGMPRLGGAGAGLGTSLTYWAIFIGHIIVMS
LHPQIKTYHIWTLERIKAPLIIEDIRLGLPIGLQIFA EVAIFA VVGLFMAKFSSIIIA
AHQAAMNFSSLMYAFPLSISTALAITISFEVGAERFQDATTYSRIGRLTAVGITS
GTLFLFLFRENVAAAMYN SAPHVAITAQFLTYSLFFQFADAYAAPVQGILRG
YKDTTKPFMIGAGSYWLCALPLAVILEKNSQLGPFAYWIGLITGIFVCGFLFNQ
RLQIKKKLYY*

Sequence description:

- A) Length: 1341 bp - 447 aa (full length gene)
- B) Shine-Dalgarno sequence present upstream of
ATG start codon, There is a potential signal
peptide sequence

ID-106

FIG. 1_{CONT'D}

28 / 110

Clone 2-4A

TTGCTAGTTTCTTCTCTAGTTTCTTGTTTCATTTTTCTTGTCATTTTCGTCGTT
GTCTTCATCAACACGAAATAAGTCTATAAACTTATCAAATAATTTCATAGA
CTTATTATATCAATTTTCAATAAAATGCTATAATAAAACCATGTCATTTTCA
TTAAAAATTAGAAATCCATACGGTGAACATACCGTTAAAGAACTCCTTGA
AGATTATTTTTTGATTCCACGTAAGATTAGACATTTTTTGCCTGTTAAAAAA
CATGACTTATAAACAATGAATTCATTAATTGGCAAACGTGTCGTCCTCAAGAA
AACGATACTATTACCTTAATCTTTGATGATGAGGATTACCCTACTAAAAAA
ATTCCTCTGGGCAGAGCAGAGCTTATTGATTGTCTTTATGAGGATGAACAT
CTTATTATCGTTAATAAACCTGAAGGTATGAAAACCTCACGGTAACCAACCA
AATGAAATAGCACTGTAAATCATGTATCTGCCTATTCTGGACAAACATGC
TATGTTGTTTCATCGCCTAGATATGGAGACCAGTGGAGCTGTTTTATTGCT
AAAAATCCATTTATACTTCCCCTTATCAATCAACGCTTAGAACGAAAAGAA
ATTGCGCTGAATATTGGGCTTTAGTTGAAGGAAAAATTTTACCTAAGCAT
CAAGTTTTGAGAGACAAAATTGGACGGAACCGTCATGACAGACGTAAACG
AATCATTGATTCTAAAAACGGTCAACATGCTATGACAATCATTGACGTTTT
GAAGTATATCCAAAATAGTAGTCTCATAAAATGCCGACTGGAAACCGGAA
GAACCCATCAAATTCGCATTCACTTATCTCATCACGGACATCCTTTAATAG
GAGATCCCCTCTACAACCCTTCTTCTAATAATGAAAGGTTAATGCTACACG
CTCACCATTGACTCTATCCCATCCATTAACCTTGCGAAACTATTAGCGTAG
AGGCCCTTCATCTACTTTTCGAGAAGGTTTTAAACAATTATAAAAAAGGAG
TTGGATAA

MLVSSLVSCSFLLVISSLSSSTRNKSINLSNNFIDLLYQFSIKCYNKTMSFSLKIR
NPYGEHTVKELLEDYFLIPRKIRHFLRVKKHVLINNEFINWQTVVQENDTITLIF
DDEDYPTKKIPLGRAELIDCLYEDEHLIIVNKPEGMKTHGNQPNELIALLNHVSA
YSGQTCYVVHRLDMETSGAVLFAKNPFIPLINQRLERKEIWREYWALVEGKF
SPKHQVLRDKIGRNRHRRRKRIIDSKNGQHAMTIIDVLKYIQNSSLIKCRLETG
RTHQIRIHLSHHGHPLIGDPLYNPSSNNERLMLHAHRLTLSHPLTCETISVEAPS
STFEKVLNNYKKGVG*

Sequence description:

- A] Length: 1029 bp - 343 aa (Full length gene sequence)
B] No obvious Shine-Dalgarno sequence upstream
of the putative TTG start codon. Possesses a
potential leader peptide sequence.

FIG. 1 CONT'D

29 / 110

ID-107

Clone 2-54

GAACTAAATGCAACTCAACCTAATAATAGAACTACCTATATTATACCCGAA
AGCAGTCATTCCATTGCAGAACACAGAGATTCCTGATAGAATCAAAGGG
TTCTTCGGTTGCATTACTTAATAGCGATGAATTTAGAAAGACAGCGGGAGA
GGATAGAGGTTTTGAAAGGGGATAAGTTGAGGTCTTTGGATATCATTCTAA
GGGAGATTTATCGACAAGTAATGTCATAGGTAATACGGACATTGCTAGTC
AGATATCGTTGGGCTTTAAAAAGAATGCGATGCAGGAACACCATCTTACT
AAAACATTCTCTCAAAAGGATGGAAAGTTATCGTCTGTTATAGAGGGGAT
GCTTGCTATTGGCAAAGAGAAAGTAGAGAAAGAAATAAAATATAGTGGTA
ATTTATGGCAAAAATTAAGCTAAGGCACACTGCCTTGTTTGCTGTGTG
ATAATTTGAATTTTGAAGATATAAAATCTTATTTTCAATATTATTGTCATCT
AAACCATCAGCTCAAATTACCTAAAGGTGCTATACTTTCTGCTAAAACAGA
AGTATATAGGGGAGGAGATTTTGGGAGAAAAAATAAAGATAATGTGTTTG
GTTACCGTATCCCTCATTATTGAAAACCCAAAAAGGAACCTTACTTGCGG
GAGCTGATGAAAGAATTGAGCAAGCTTGTGATTGGGGAAACATAGGAATG
GTTATTCGCCGTAGTGAGGATGATGGTGTCACTTGGGGAAAAAGAGAAAC
TATTGTCAATCTCCGTAATAACCCTAGAGTTCGCTAGTTACTAGTGGTGA
CTATAGTGGCTCACCTATTAATATGGATATGGCATTAGTTCAAGATACTAG
CTCCAAGACGAAACGTATTTTTCAATATATGATATGTTTCCAGAAGGAAG
AGGCGTTATTAGTATTGCTAACACACCTGAAAAAGAATATACCCAAATCG
GAGGACAGTCTTATCTTAATTTATATAATAATGGAAAGAAATCGAAGGTTT
TACTATCCGTGACAAAGGTATTGTATATAATTTTAAAGGGAAAAAGACTG
ATTATCATGTTATAACAGAACTACTAAAAGTGACCATTCAAATCTAGGGG
ATATTTATAAGGGAAAAACAGCTACTTGAAATATATATTTTACAAAACATA
AAACGTCACCATTTTCGTTTAGCAAAATCAAGCTATGTGTGGATGTCATATA
GCGATGATGATGGTAGGACATGGTCATCACCTAGAGATATAACAGCAAGT
CTTCGTCAGAAAGGCATGAAATTTTTGGGAATAGGACCTGGAAAAGGTAT
AGTTTTTAAATGGGGGCCACACGCTGGTTCGTATTATTCTCCTGCCTATTCT
ACGAATTGGAAATCTCATCTAAGAGGTTCAATCTTCACGCCTAATTTAT
TCAGACGACCATGGAAAAACGTGGCATACTGGAAAAGCAGTTAATGATAA
CCGTATACTTTCTAATGGTGAAAAAATTCACCTCTTAACAATGGATAATAA
AAAAGAACAAAATACAGAATCCGTACCCGTTCAATTGAAAAATGGGGACA
TTAAGTTATTTATGAGGAATCTAACTGGTAACCTAGAAAGTAGCCACAAGTA
AAGACGGCGGGGAGACTTGGCAAAACCATGTTAAACGATATAAGGAAATT
CATGATGCTTACGTCCAATATCAGCTATTTCGCTTTGAGCATGACAAAAA
GAGTATATTTTATTAGTGAATGCTAATGGGCCAGGGAAGAAGTGCCAAGA
TGGATATGCACGTCTAGCGCAAGTTAATCGAAATGGTAGTTTTAAGTGGTT
ATATCACCATCACATTCAAGATGGTTCGTTTGCTTACAACCTCTGTTCAACA
ACTTAATAATGATCAATTTGGTGTCTTTATGAACATAGAGAAAAACATCA

FIG. 1 CONT'D

SUBSTITUTE SHEET (RULE 26)

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AAATAGTTTTACTTTAAATTACAAAGTTTTTAATTGGAGTTTTCTTAGTCAA
AATACAGAGAAGCAAGGCACTTTATGGGAGAAAATGGCAGCAAATTGGCA
TGTTTTGTTTAAATTTTATTTATGA

ELNATQPNNRTTYIIPESHSIAEQQRFLIESKGSSVALLNSDEFKRTAGEDRGF
ERDKLRSLDIIPKGD LSTSNVIGNTDIASQISLGFKKNAMQEHLTKTFSQKDG
KLSSVIEGMLAIGKEKVEKEIKYSGNLWQKLKAKAHCLVCCVDNLNFEDIKS
YFYYYCHLNHQLKLPKGAILSaktevyrGGDFGRKNKDNVFGYRIPSLLKTQ
KGTLLAGADERIEQACDWGNIGMVIRSEDDGVTWGKRETIVNLRNPNRVPL
VTSGDYSGSPINMDMALVQDTSSKTKRIFSIYDMFPEGRGVISIANTPKEYTQI
GGQSYLNLNNGKKS KSVFTIRDKGIVYNFKGKKT DYHVITETTKSDHSNLGDI
YKKGQLLGNIYFTKHKTSPFRLAKSSYVWMSYSDDDGR TWSSPRDITASLRQ
KGMKFLGIGPGKGIVLKWGPHAGRIIPAYSTNWKSHLRGSQSSRLIYSDDHG
KTWHTGKAVNDNRILSNGEKIHSLTMDNKKEQNTESVPVQLKNGDIKLFMRN
LTGNLEVATSKDGGETWQNHVKRYKEIHDA YVQLSAIRFEHDKKEYILLVNA
NGPGKKCQDGYARLAQVNRNGSFKWLYHHHIQDGSFA YNSVQQLNNDQFG
VLYEHREKHQNSFTLNYKVFNWSFLSQNTEKQGTLEWKMAANWHVLFKFYL
*

Sequence description:

- A] Length: 2052 bp - 684 aa (partial gene sequence)
B] N-terminus has yet to be determined

ID-108

Clone 2-61

ATGCCTAAATTAATCGTATCTTTCCTCTGCATTTTATTATCCCTGACTTGTG
TAAACTCTGTGCAAGCTGAAGAACATAAAGATATTATGCAAATTACCCGA
GAAGCCGGATATGATGTAAAGATATTAATAAACCTAAAGCGTCTATCGTT
ATTGACAATAAAGGTCATATTTTGTGGGAAGATAACGCCGATTTAGAACGT
GATCCCGCTAGCATGTCTAAAATGTTTACTTTATATTTACTATTTGAAGACT
TAGCTAAAGGAAAAACAAACCTCAACACCACAGTGACTGCAACAGAAACA
GACCAAGCCATAAGTAAGATTTATGAAATTAGTAATAACAATATTCATGCT
GGGGTTGCTTATCCTATTCGTGAAGTACTATGACGGCTGTCCCGTCA
TCTAATGTAGCAACTATTATGATTGCTAACCCTTATCACAAAACAATCCT
GACGCCTTTATTAACGAATCAATGAAACCGCCAAGAACTCGGTATGAC
AAAAACTCACTTTTATAACCCAGTGGGGCGGTAGCGAGTGCTTTTAATGG
ACTTTACTCCCCAAAAGAATACGATAACAATGCTACTAACGTTACGACTGC

FIG. 1_{CONT'D}

31 / 110

ACGTGATCTATCAATTTTAACTATCATTTTCCTTAAAAAATACCCTGATATA
CTGAACTATACAAAATATCCTGAAGTCAAGGCCATGGTCGGAACCTCCTTAT
GAAGAAACATTTACAACCTTATAACTACTCTACCCCCGGCGCTAAATTTGGA
TTAGAAGGAGTAGATGGCTTAAAAACTGGTTCTAGCCCTAGCGCTGCTTTT
AATGCCTTAGTTACAGCTAAACGCCAGAATACTCGCTTGATAACTGTGGTT
TTAGGAGTTGGCGATTGGTCAGACCAAGACGGAGAGTACTATCGTCATCC
GTTTGTCAACGCTCTTGTAGAAAAAGGTTTTAAAGACGCTAAAAATATTTT
TTCTAAAACTCCTGTATTAAAAGCCGTTAAACCTAAAAAAGAAGTTACTAA
AACCAAACTAAATCTATTCAAGAACAGCCTCAAACAAAAGAACAGTGGT
GGACAAAACAGATCAATTTATCCAATCACATTTTGTATCTATTTTAATTG
TTCTGGGCACCATCGCTAGCCTTTGTCTTTTAGCTGGGATAGTATTACTTAT
AAAGCGCTCTAGATAA

MPKLIVSFLCILLSLTCVNSVQAEHKDIMQITREAGYDVKDINKPKASIVIDN
KGHILWEDNADLERDPASMSKMFTLYLLFEDLAKGKTNLNTTVTATETDQAI
SKIYEISNNNIHAGVAYPIRELITMTAVPSSNVATIMIANHLSQNNPDFAIKRINE
TAKKLGMTKTHFYNPSGAVASAFNGLYSPKEYDNNATNVTTARDLSILTYHF
LKKYPDILNYTKYPEVKAMVGTPYEETFTTYNYSTPGA KFGLEGVDGLKTGS
SPSAAFNALVTAKRQNTRLITVVLGVGDWSDQDGEYYRHPFVNALVEKGFK
DAKNISSKTPVLKAVKPKKEVTKTKTKSIQEQPQTKEQWWTKTDQFIQSHFVS
ILIVLGTIASLCLLAGIVLLIKRSR*

Sequence description:

- A] Length: 1188 bp - 396 aa (full length gene)
- B] Shine Dalgarno sequence present upstream of
ATG start codon, possesses a potential signal
peptide

ID-109

Clone 45

ATGACTGAAAAATATTATAATTGGGCAACGCTTGGAACCGGCGTTATTGCC
AACGAATTAGCCCAAGCACTGGAAGCACGTGGACAAAAATTATATTCTGT
AGCTAATAGAACTTACGACAAAGGACTTGAATTTGCTAACAAATATGGTA
TCCAAAAAGTTTATGATCACATAGATCAAGTATTTGAAGACCCTGAAGTGG
ATATCATTTATATCTCTACTCCCCACAATACTCACATCTCATTTTTACGAAA

FIG. 1_{CONT'D}

32 / 110

GGCTTTAGCAAATGGTAAGCACGTTCTTTGCGAAAAATCTATTACTTTAAA
TAGTACTGAGCTTAAAGAAGCCATAGATTTAGCCGAAACTAACCATGTTGT
CTTAGCTGAAGCCATGACTATTTTTTCATATGCCAATTTACCGCCAATTAAA
AACATTAGTTGATAGTGGAATAATTAGGACCGTTAAAAATGATTCAAATGA
ATTTGGAAGTTATAAGAATATGATATGACTAACCGTTTTTTTCAGTCGTG
ACCTAGCAGGCGGTGCTTTGCTGGACATTGGTGTTTATGCACTTTCTTGAT
TCGCTGGTTTATGTCAGAAGCACCTCACAACTTACCTCTCAAGTTACATT
TGCACCAACAGGGGTTGATGAACAAGTTGGTATCCTACTAACCAACCCAG
CAAATGAGATGGCGACTGTCAGCCTTAGTTTACATGCAAAACAACCTAAA
CGAGCAACTATCGCTTACGATAAAGGCTACATTGAACTTTTTGAATATCCG
CGAGGACAAAAGGCAGTTATTACTTATACTGAGGATGGGCATCAAGATAT
TATCGAAGCTGGCAAACTGAAAATGCTCTCCAATATGAGGTAGCTGATA
TGGAAGAAGCCATTTTCAGGAAAACTAACCACATGTACTTAACTATACC
AAAGATGTTATGGATATCATGACACAGCTACGTCAAGAATGGGGATTTAC
CTACCCAGAAGAAGAAAAATGA

MTEKYYNWATLGTGVIANELAQALEARGQKLYSVANRTYDKGLEFANKYGI
QKVYDHIDQVFEDPEVDIIYISTPHNTHISFLRKALANGKHVLCEKSITLNSTEL
KEAIDLAETNHVVLAEAMTIFHMPYRQLKTLVDSGKLGPLKMIQMNFSGYK
EYDMTNRFFSRDLAGGALLDIGVYALSCIRWFMSEAPHNITSQVTFAPTGVDE
QVGILLTNPANEMATVSLSLHAKQPKRATIAYDKGYIELFEYPRGQKAVITYT
EDGHQDIIEAGKTENALQYEVADMEEAISGKTNHMYLNYTKDVMDIMTQLR
QEWGFTYPEEEK*

Sequence description:

- A) Length: 984 bp - 328 aa (full length gene)
- B) Shine Dalgarno sequence present upstream of
ATG start codon, possesses a potential signal
peptide

ID-110

Clone 2-2

GTGTATTCTCCTGTAAATCTTCTAAAGGAAAAGTGATATTGTTAAAAAGT
GATTTTCTAAAGAGCTTCATAGAAAGGAGAGGAAATATTTGTTTT

MYSPVKSSKGKVILLKSDFLKSFIERGNICF

FIG. 1 CONT'D

33 / 110

Sequence description:

A] Length: 96 bp - 32 aa (partial sequence)
B] GTG start codon - no obvious Shine-Dalgarno
sequence
Possesses a potential signal peptide

ID-111

Clone 2-3

AAATACTGTATCATTGCAACCTCAAATGCAGGTTTTGGAAACGAAGCATT
ACAGGTGACAGCGATAAAGACTTGAAAATTATGGAACGAATTTCTCCATA
TTCCGTCAGAAATTTCTAAATCGTTTCAATGGTGTTATTGAATTCTCTCAC
CTAAGCAAAGATGACTTAAGCGAAATTGTAGATTTGATGCTTGATGAAGTT
AACCAAACAATTGGCAAAAAAGGAATTGACCTTGTGGTAGATGAAAATGT
TAAATCACACTTAATTGAACTGGGTTATGACGAAGCAATGGGAGTACGTC
CATTGCGCCGTGTCATCGAGCAAGAAATTCGAGATCGCATCACAGACTACT
ATCTCGATCATAACAGACGTTAAACACCTAAAAGCTAATTTGCAAGATGGCC
AAATCGTCATTTCTGAAAGATAA

KYCHATSNAFGNEAFTGDSKDLKIMERISPYFRPEFLNRFNGVIEFSHLSKD
DLSEIVDLMLDEVNQITIGKKGIDLVDENVKSHLIELGYDEAMGVRPLRRVIE
QEIRDRTDYILDHTDVKHLKANLQDGGQIVISER*

Sequence description:

A] Length: 429 bp - 143 aa (partial sequence)
B] N-terminus yet to be elucidated. This gene
was not in frame with nuc

ID-112

Clone 2-5

FIG. 1 CONT'D

34 / 110

ATGTCAATGAATTTTTCATTTTACCACAATATTGGTCCTATTTTAATTATG
GTGTGATGGTAACCATTATGATTTCAACATGTGTTGTTTTTTTGGAACTAT
TATAGGCGTGTTAATTGCTTTAGTAAAGCGTACTAATTTACATTTTCTCACA
ATATTAGCTAATTTCTATGTATGGGTATTTTCGTGGGACACCGATGGTAGTT
CAAATTATGATTGCTTTTCGCATGGATGCATTTTAACAATTTACCAACAATT
AGCTTTGGTGTTTTAGATTTAGATTTTACACGACTTTTACCTGGTATCATT
TCATTTCTTAAATAGTGGTGCCTATATTTTCGGAAATTGTACGTGCAGGGA
TTGAGGCTGTACCATCTGGACAAATAGAAGCAGCTTACTCGTTGGGGATT
GACCTAAAAATACACTTCGCTATGTTATCTTACCCCAAGCTTTTAAAAATA
TTTTACCTGCTCTAGGGAATGAATTTATTACAATTATTAAAGATAGTGCTCT
CCTTCAAACTATTGGTGTTCATGGAATTATGGAACGGAGCACAATCAGTTGT
AACGGCTACTTACTCACCAGTTGCACCGTTATTATTTGCAGCATTTTACTAT
TTAATGTTGACAACGATTCTCTCAGCTTTGTAAACAAATGGAGAAATAT
CTTGGGAAAGGGGTAAAAATAGATGGTTGA

MSMNFSFLPQYWSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTIL
ANFYVWVFRGTPMVVQIMIAFAWMHFNNLPTISFGVLDLDFTRLLPGIIISLNS
GAYISEIVRAGIEAVPSGQIEAAYSLGIRPKNTLRYVILPQAFKNILPALGNEFITI
IKDSALLQTIGVMELWNGAQSVVTATYSPVAPLLFAAFYYLMLTTILSALLKQ
MEKYLKGVKIDG*

Sequence description:

- A] Length: 699 bp - 233 aa (full length gene)
- B] Shine-Dalgarno sequence preceded the 'ATG' start codon. Possesses a potential leader peptide sequence.

ID-113

Clone 2-7

ATGAAAGACCTATTACGAAATAGTCTAGAGCAAAGTGGAAATTTAAGTTT
TCAAGATATGATTTTACATATTCTTGTAGCAGCTTTATTGAGTGTAGTTATT
TATGTTTCCTATGCTTATACGCATAGTGGAAGTGCCTATAGTAAAAAGTTT
AATGTTTCATTAATGACATTGACGGTCTTGACTGCAACAGTAATGACCGTT
ATTGGTAATAATGTAGCCTTGTCATTGGGTATGGTCGGTGCCTTGTCAGTT
GTTCTGTTTATAGGACAGCCATAAAAGATTCAAGAGATACAGTTTATATTTT
TGGACCATAGTTGTTGGTATCTGTTGTGGTGTCCGTGACTATGTGGTAGCT

FIG. 1 CONT'D

35 / 110

GCATTAGGAAGTAGCGTTATCTTTATCTTATTATGGGTTATGGGACGTGTT
AAAAACGAGAATCGTATGTTATTGATTGTGAAGTGCGATAGAACACTAGA
AGTTGATTTAGAAGGAATTTTCTTCCAATATTTTGACGGAAAAGCTGTTCA
GCGTGTTAAAAATTCAACAATACTATTGAAATGATTTTCGAAATCTC
TAGAAAAGATTACGATAAGCAACTCCATGTAGATAATCAGTTAACTGAAA
AAGTGTACCAATTGGGAAATATTGATTATTTCAACATTGTTAGCCAAAGCG
ACGAAATCAATGGGTAG

MKDLLRNSLEQSGNLSFQDMILHILVAALLSVVIYVSYAYTHSGTAYSKKFNV
SLMTLTVLTATVMTVIGNNVALSLGMVGALS VVRFR TAIKDSRDTVYIFWTIV
VGICCGVGDYVVAALGSSVIFILLWVMGRVKNENRMLLIVKCDRTLEV DLEGI
FFQYFDGKAVQRVKNSTTNTIEMIFEISRKYDKQLHVDNQLTEKVYQLGNID
YFNIVSQSDEING*

Sequence description:

- A) Length: 678 bp - 226 aa (full-length gene)
- B) ATG start codon is preceded by a Shine-Dalgarno sequence-Possesses a potential leader peptide sequence

ID-114

Clone 2-8

AAAAATTCATTTTAGATTTCATTTTACGACTATATACTCAGAAGTACCAAAC
CTAATCCAAGGTTTGAAAAAAGAAAGAAGTCAGTATGACAACTAT
AAAAACAACTTTAAAGATGAGGCTATACGTGTTGAAGAGACAACAAAAGA
ATCATTTTACGATGTTGATATTGCCTTGTTTTAGCTGGTGGATCTATTTCA
GCAAAGTTCGCTCCTTATGCAGTAAAGTCTGGAGCAGTTGTAGTAGATAAC
ACGTCATATTTTCGTCAGAATCCTGATGTTCCACTAGTTGTTCCCTGAAGTAA
ATGCTCATGCCATGATTGGTCATAATGGTATCATAGCTTGTCCTCAATTGTTT
TACTATTCAAATGATGATTGCTTTAGAGCCCATTCGTCAAAAATGGGGGAT
AGAGCGTGTTATAGTTTCCACCTATCAAGCTGTTTCGGGTTACAGGTGCACG
TGCTGTTGAAGAACTAAGGAACAGTTGAGACAAGTTTT

KFILD SFYDYILRSTKPNPRFEKRKKEVSMTNYKNNFKDEAIRVEETTKESFYD
VDIALFSAGGSISAKFAPYAVKSGAVVDNTSYFRQNPDPVPLVVPEVNAHAMI
GHNGIIACPN CSTIQMMIALEPIRQKWGIERVIVSTYQAVSGSGARAVEETKEQ
LRQV

FIG. 1_{CONT'D}

36 / 110

Sequence description:

- A] Length: 499 bp - 165 aa (partial sequence)
B] N-terminus has yet to be determined

ID-115

Clone 2-9

ATGACAAATGAATTGATAATGCAAGCTTTTGAGTGGTATTTACCTAGTGAT
GGGAATCACTGGAAGAAATTAGAGGAGTCTATATCAGACCTTAAAAAACT
TGGAATTAGTAAAATCTGGTTACCACCAGCATTTAAGGGAAGTAGCAGTG
ATGATGTAGGATATGGTGTATATGATCTCTTTGATTTAGGAGAATTTGACC
AGAATGGAACAATTAGAACAAAATATGGTAGGAAAGAAGAGTATCTAAA
GCTTATTAAGTCGTTAAAGGCAAATGGCATTAAACCGTTTGCAGATATCGT
TCTTAACCATAAAGCCAATGGTGATCATAAAGAAAAATTTCAAGTCATCA
AAGTCAATCCTGAAAATCGTCAAGAAGCATTAAAGTGAACCCCTATGAGATT
GAAGGATGGACGGGATTTGATTTCCAGGTAGACAGGGTGAGTACAATGA
TTTT

MTNELIMQAFEWYLPDGNHWKKLEESISDLKKLGISKIWLPPAFKGTSSDDV
GYGVYDLFDLGEFDQNGTIRTKYGRKEEYLKLIKSLKANGIKPFADIVLNHKA
NGDHKEKFQVIKVNPNRQEALSEPYEIEGWTGFDFPGRQGEYND

Sequence description:

- A] Length: 456 bp - 152 aa (partial sequence)
B] ATG start codon is preceded by a Shine-
Dalgarno sequence, no leader peptide sequence.

ID-116

Clone 2-10

FIG. 1 CONT'D

37 / 110

ATGGAGGTTCTTATGAAGAAAGTGTTAGTAAGTAGTCTTTTGGTTTTAGGG
ATTACGATAACGTTACAACCAGTAGTTGAGGCTAAGGGGCCAAAAGTAGC
TTATACACAAGAGGGAATGACTGCTCTTTCGGACACAAATAAAGATAAAG
TCACTACTATTTCTATTGACGAGATTCAAAAAAGCTTAGAAGGTAAGAAGC
CGATTACTGTTAGTTTTGATATTGATGATACTGCTTTTCAGTAGTCAATA
TTTTCAATATGGTAAAGAATATGTAACCTCGGATCGTTTGATTTTCTTCAT
AAACAAAAATTCTGGGATCTTGTGCAAAACGAGGAGATCAAGATTCCAT
TCCCAAAGAATATGCTAAAAAATTAATTGCTATGCATCAAAAACGAGGAG
ATAAAATTGTTTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAG
GGCGAGGTTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTTGTA
CCATCTGAT

MEVLMKKVLVSSLLVLGITITLQPVVEAKGPKVAYTQEGMTALSDTNKDKVT
TISIDEIQKSLEGKKPITVSFDIDDTLFSSQYFQYGKEYVTPGSFDLHKQKFW
DLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGSMYKEGEVDKTA
KALAKDFKFVPSD

Sequence description:

- A) Length: 516 bp - 172 aa (partial sequence)
- B) ATG start codon is preceded by a Shine-Dalgarno sequence, Possesses a leader peptide sequence.

ID-117

Clone 2-17

ATGCTTAAAAGATTATTTACTGAAGATGGGGAATTGACAAAGATTAGTCGT
CGTTTCGTTTGATGTTAGTGTTATCTATTGTCTTATTATTGTCAGGATGT
GTTTTGGGCCTCAAATTATGATTGAGGGGTATCAACTCCGAATGTTTCAGC
GCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTTAATTCTTTTCGTAGTTT
AGATCAGCTAACTAGCTTTAAAGAGATTCTTTGGGTTATTGGTCAAAATGT
AGTGAATATTTTACTGCTGTTTCCTCTCATTATAGGGTTACTATCCCTAAAG
CCAAGTTTACGGAAATATAAAAGCGTTATATTACTTGCTTTCTTGATGTCTC
TTTTCATAGAGTGTACTCAAGTTGTTTTAGATATTTTAATAGATGCTAATCG
GGTTTTTGAAATCGACGATCTATGGACAAATACCTTAGGCGGTCTTTTCGC
CCTATGGAGTTATCGAAACATAAAAGGTTGGCTTCTAACTATTAGAAAATG
A

FIG. 1 CONT'D

38 / 110

MLKRLFTEDGELTKISRRFVWMLVVIYCLIIVRMCFGPQIMIEGVSTPNVQRF
RIVALLVPFNSFRSLDQLTSFKEILWVIGQNVVNILLFPLIIGLLSLKPSLRKYK
SVILLAFMLSLFIECTQVVLIDILIDANRVFEIDDLWTNTLGGPFALWSYRNIKG
WLLTIRK*

Sequence description:

- A] Length: 516 bp - 172 aa (full-length gene)
B] ATG start codon is preceded by an Shine-
Dalgarno sequence. Possesses a potential leader
peptide sequence. C-terminus need further
confirmation.

ID-118

Clone 3-3

ATGAAAAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTTCG
TATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA
ATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGG
CAATTATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAAACT
GAAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATT
TAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAAGAACAAGATATT
CCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTCAAGTGTGGAA
ACCTTGCAGATCTCTCATTATTTTGTGAAATTTTAACTGGTGTTCGGGAT
TCGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATT
CTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGG
AGGTTGCTCAAAATGCTGGTATAAAATCCATAAACTTAAGGTTAGAGAATT
CCAAAGAAAACATAAATTTCAAGTCTCAAAGATATAATATCACTTGATT
TCACTCGTTTGGATTAA

MKKLTFIWDLDGTLIDSYPIMEALEETYRHFGLIFDKELIHEYILQESVGQLL
VNLSEEEQIPHEKLKAYFTKEQESRDSKIHLMPLYAKEILEWTKEQDIPNFMYTH
KGASTHSVLETLQISHYFDEILTGVS GFERKPHPQGINYLVKRYSLDKSMTYYI
GDRPLDLEVAQNAGIKSINLRLNSKENYNISSSLKDIISLDFTRLD*

Sequence description:

- A] Length: 627 bp - 209 aa (Possible Full-length gene)

FIG. 1 CONT'D

39 / 110

BJ ATG start codon is preceded by an possible
Shine-Dalgarno sequence. No obvious leader
peptide sequence.

ID-119

Clone 3-7

ATGGAAAAAGAAAAAAATTAGGTCTTTTACCACTAACAATGCTTGTCATT
GGCTCTCTTATCGGTGGCGGAATCTTTGATTAAATGCAAAATATGAGTTCC
AGAGCCGGTTTGGTACCAATGCTTATTGCTTGGGTAATTACTGCTATCGGG
ATGGGAACCTTTCGTTTTAAGTTTTCAAAATTTATCTGAAAAAGGCCGGAC
CTAACAGCTGGAATCTTTAGTTACGCTAAAGAGGGGTTTGGAACTTTATG
GGATTAACTCTGCATGGGGTTATTGGTTATCAGCTTGGCTTGGAATGTT
GCCTACGCTGCACTCTTATTCAGTTCACCTCGGTTATTTCTTTAAATTCCTTG
GTAATGGAAATAATATCATCTCAATTATTGGAGCAAGTATAGTTATTTGGG
TTGTCCATTTCTTAATTTTAAGAGGTGTTAATACAGCTGCATTTATTAATAC
CGTAGTTACCTTTGCAAAATTAGTACCTGTTATTATTTTCTTAATTCAGCG
TTATTAGCTTTCAAATTTAACATTTTTAGTCTTGATATCTGGGGAAATGGAT
TACATCAATCAATTTCAACCAAGTCAATTCAACTATGAAAACCGCTGTTT
GGGTATTTATTGGTATTGAGGGCGCCGTTGTCTTCTCAGGTCGTGCTAAAA
AACACTCTGATATTGGTAAAGCAAGTATCCTAGCATTATTCAGTATGATTT
CACTTTATGTATTGATTTCTGTTTTATCACTTGGTATCATGTCACGTCCAGA
ACTTGCAAACTTAAAAACACCAGCTATGGCTTACGTTCTAGAAAAAGCTGT
TGGTCACTGGGGTGCTATCTTAGTTAACCTTGGTGTATCATTTTCAGTATTT
GGCGCTATTCTTGCTTGGACTTTATTTGCAGCAGAATTACCATATCAAGCT
GCTAAAGAAGGTGCTTTTCCTAAATTTTTTGCAAAAGAAAAATAAAAAACA
AGCTCCAATCAACTCACTCTTAGTCACTAATCTTTGTGTACAAGCATTCTTA
ATCACGTTCTTATTCACACAAAGTGCTTATCGTTTTGGTTTTCGCATTAGCAT
CATCTGCTATCTTAATTCCTTATGCTTTTACAGCACTATATCAATTACAATT
CACACTCCGTGAGGATAAGTCAACTCCAGGACATCAAAAGAATTTAATTA
TCGGTATCCTCGCTACAATCTATGCTGTTTACCTTATCTACGCTGGTGGTTT
TGATTACTTACTTTTGACAATGATTGCTTATACTCTAGGTATGATTCTCTAT
ATTAAAATGAGAAAAGATGACAAGCTTGGCGTAATCATGGTCATAGCTGT
TTCCAGTGTGAAATTGTTATCC

MEKEKKLGLLPLTMLVIGSLIGGGIFDLMQNMSSRAGLVPMLIAWVITAIGMG
TFVLSFQNLSEKRPDLTAGIFS YAKEGFGNFMGFNSAWGYWLSAWLGNVAY
AALLFSSLGYFFKFFGNGNNIISHIGASIVIWVVHFLILRGVNNTAAFINTVVTFK
LVPVIIFLISALLAFKFNIFSLDIWGNGLHQSIFNQVNSTMKTAVWVFIGIEGAV

FIG. 1 CONT'D

40 / 110

VFSGRAKKHSDIGKASILALFTMISLYVLISVLSLGIMSRPELANLKTPAMAYV
LEKAVGHWGAILVNLGVIIISVFGAILAWTLFAAELPYQAAKEGAFPKFFAKEN
KNKAPINSLLVTNLCVQAFLITFLTQSA YRFGFALASSAILIPYAFTALYQLQF
TLREDKSTPGHQKNLIIGILATIYAVYLIYAGGFDYLLLTMIAYTLGMILYIKMR
KDDKLGVMVIAVSSVKLLS

Sequence description:

- A] Length: 1356 bp - 452 aa (partial sequence)
B] ATG start codon is preceded by an possible
Shine-Dalgarno sequence. Possesses a potential
leader peptide sequence.

ID-120

Clone 3-8

ATGAAATTTGAAAAACGGCAGGTCTATTATGTTGTCATAACATTTGCTATT
TGCTATGCTATACAGGCTTATTGGGGAGCTGTTTCTAATATTTAACTACGC
TTCATAAGGCAATATTTCTTTTTTGATGGGAGCTGGAATTGCCTATATTAT
TAATATTGTAATGTCAGTCTATGAGCGATTATATATAAAAGCTTTTTAAAGG
ATCTAGACTATTAATGGCAATCAAGCGTAGTGTTTCTATGATTTTATCCTAT
GCAACTTTTATTGGTTTAATTGTCTGGCTATTTTCAATTGTCATTCCAGATT
TGATTCTAGTTTGAGTTCTTTATTGGTTATTGATACCGGAGCACTTGCTAA
ATTGGTTAATAATCTCAATGAAAATAAACAAATTTCTGAGGCTTTAAATTA
TATGGGAACAGATAAAGACTTAGTTTCTACTTTAAGTGTTATAGCCAGCA
GATTTTGAAGCAAGTTTTATCTGTTTTAACAATTTACTAACCTCAGTTTCC
TCTATTGCGGCAACACTTCTGAATGTTTTGTTAGTTTTATTTTTCAATTTA
CGTTTTGGCAAACAAGGAGCAGTTGGGACGTCAATTTAATTTGTTAATTGA
TACCTATTTAGGTTCAACAGGCAAAACATTCCATTACGTTTCGTCATATCCTT
CATCAACGTTTCCATGGTTTTTTTGTAAGCCAACTTTAGAAGCTATGATTT
TAGGAAGTTTGACGGTTATTGGTATGTTGATCTTCCAATTTCTTATGCTTT
AACAGTTGGGGTTTTAGTTGCTTTTACAGCTCTAATACCGGTTGTGGGAGC
CTACATTGGTGTTACAATCGGTTTCATCTTAATTGCTACTGAATCGCTTACT
GAAGCATTCTTGTTTCTTTTCTTGATCCTTTTACAACAATTTGAGGGAA
ATGTCATTTATCCGAAAGTTGTCGGTGGATCGATTGGACTGCCTTCTATGT
GGGTTTTAATGGCTATTACTATCGGAGGTGCTTTATGGGGGATCTTAGGCA

FIG. 1_{CONT'D}

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TGTTACTTGCTGTTCCCTGTTGCAGCTACTATCTATCAGATTGTAAAAGATCA
TATTATCAAGCGACAAACGCTTAGAAATCGTGCACGAACCTATCGTTAA

MKFEKRQVYYVITFAICYAIQAYWGAVSNILTLHKAIFPFLMGAGIAYINI
VMSVYERLYIKLFKGSRLMAIKRSVSMILSYATFIGLIVWLFSSIVIPDLISSLS
LLVIDTGALAKLVNNLNENKQISEALNYMGTDKDLVSTLSGYSQQILKQVLSV
LTNLLTSVSSIAATLLNVFVSFISYVLANKEQLGRQFNLLIDTYLGSTGKTFH
YVRHILHQRFHGFFVSQTLEAMILGSLTVIGMLIFQFPYALTVGVLVAFTALIP
VVGAYIGVTIGFILATESL TEAFLFVLFLILLQQFEGNVIYPKVVGGSIGLPSM
WVLMAITIGGALWGILGMLLAVPVAATYQIVKDHIKRQTLNRARTYR*

Sequence description:

- A] Length: 1134 bp - 378 aa (full-length gene)
- B] ATG start codon is preceded by an typical
Shine-Dalgarno sequence. Possesses a potential
leader peptide sequence.

ID-121

Identical to ID-68, as described in WO 00/06736

ID-122

Clone 3-16

GTGATTACAATTAAAAAGGAATCTGTTATCAAACCTATTGAAGTATGCTTTT
GGCATTATAATGGGATTTATTATCTTAGCTATTGTAATAGGTGGGCTCCTA
TTTGCACTACTACGTTAGTCGTTCTCCGAAATTAACCGATCAAGCTTTAAAA
TCCGTTAACTCTAGTTTGGTTTATGATGGTAATAATAAACTTATTGCCGATT
TAGGCTCAGAAAAGCGTGAAAGTGTTAGTGCGGATAGCATTCCACTAAAT
TTGGTTAACGCTATCACTTCTATAGAAGATAAACGTTTCTTTAAACATAGA
GGTGTCGATATTTATCGTATTTTAGGTGCAGCTTGGCATAACCTTGTAGTA
GTAATACGCAAGGTGGTTCAACCCTTGATCAACAGTTGATTAACTGGCTT
ACTTTTCTACCAATAAATCTGACCAAACGTTAAACGTAAATCACAGGAA
GTTTGGCTTGGCCTTCAAATGGAGCGTAAATACACCAAAGAAGAAATTCTT
ACTTTCTATATTAATAAAGTTTATATGGGAAATGGGAATTATGGTATGAGA

FIG. 1 CONT'D

42 / 110

ACAACAGCTAAATCATACTTTGGTAAAGACCTAAAGGAATTATCTATTGCA
CAACTTGCTTTGCTCGCTGGTATTCCTCAAGCACCTACACAATATGACCCTT
ATAAAAACCCAGAATCTGCTCAAACAAGACGTAATACCGTTCTTCAGCAG
ATGTATCAAGATAAAAAACATTTCTAAAAAGGAATACGACCAAGCTGTTGC
AACTCCAGTAACTGATGGCTTAAAAAGAATTAAAGCAAAAATCTACTTATCC
AAAATATATGGATAACTACTTAAAAACAAGTTATTAGTGAAGTTAAACAAA
AACTGGTAAAGATATCTTTACTGCTGGGCTAAAAGTGTATACTAATATCA
ACACTGATGCACAAAAACAACCTATATGACATCTACAACAGTGATACTTAC
ATCGCTTATCCAAACAATGAATTACAAATAGCATCTACCATCATGGATGCG
ACTAATGGTAAAGTCATTGCACAATTAGGCGGGCGTCATCAGAATGAAAA
TATTTCAATTTGGGACAAATCAATCTGTCTTAACAGACCGCGATTGGGGTTC
TACAATGAAACCTATCTCAGCTTATGCACCTGCTATTGATAGTGGTGTCTA
TAATTCAACAGGTCAATCATTAACGACTCAGTTTACTACTGGCCTGGTAC
TTCTACTCAACTATATGACTGGGATCGTCAATATATGGGTTGGATGAGTAT
GCAGACCGCTATTCAACAATCACGTAACGTCCCTGCTGTCAGAGCACTGA
AGCCGCTGGATTAGACGAAGCAAAATCTTTCCTTGAAAAATTAGGCATAT
ACTATCCAGAAATG

MITIKKESVIKLLKYAFGIIMGFIILAIVIGLLFAYYVSRSPKLTQALKSVNSS
LVYDGNKLIADLGSEKRESVSADSIPLNLVNAITSIEDKRFFKHARGVDIYRILG
AAWHNLVSSNTQGGSTLDQQLIKLAYFSTNKSDQTLKRKSQEVWLALQMER
KYTKEEILTFYINKVYMGNGNYGMRTTAKSYFGKDLKELSIAQLALLAGIPQA
PTQYDPYKNPESAQTRRNTVLQQMYQDKNISKKEYDQAVATPVTDLKELK
QKSTYPKYMDNYLKQVISEVKQKTGKDIFTAGLKVYTNINTDAQQLYDIYN
SDTYIAYPNNELQIASTIMDATNGKVIAQLGGRHQNENISFGTNQSVLTD RDW
GSTMKPISAYAPAIIDSGVYNSTGQSLNDSVYYWPGTSTQLYDWD RQYMGWM
SMQTAIQSRNVPVAVRALEAAGLDEAKSFLEKLGIIYPPEM

Sequence description:

- A) Length: 1386 bp - 462 aa (partial sequence)
- B) GTG start codon is preceded by an
typical Shine-Dalgarno sequence. Possesses a
potential leader peptide sequence.

ID-123

Clone 3-17

FIG. 1 CONT'D

43 / 110

ATGGCTAATGTATATGATTTAGCAAATGAATTAGAACGTGCTGTTTCGTGCT
TTACCAGAATACCAAGCAGTTTTAACTGCAAAAGCAGCTATTGAAAATGA
TGCGGATGCACAAGTGCTTTGGCAAGACTTTTTGGCTACCCAATCAAAAGT
TCAAGAAATGATGCAATCTGGCCAAATGCCAAGTCAAGAAGAACAAGATG
AAATGTCTAAACTTGGGGAAAAAATTGAATCCAATGACCTTTTAAAAGTTT
ATTTTGACCAACAACAACGGTTGTCTGTCTATATGTCTGATATCGAAAAAA
TTGTCTTTGCACCCATGCAGGACTTGATGTAA

MANVYDLANELERAVRALPEYQAVLTAKAAIENDADAQVLWQDFLATQSK
VQEMMQSGQMPSQEEQDEMSKLGEKIESNDLLKVYFDQQRLSVYMSDIEKI
VFAPMQDLM*

Sequence description:

- A) Length: 336 bp - 112 aa (full length sequence)
- B) ATG start codon is preceded by an
typical Shine-Dalgarno sequence. No obvious
potential leader peptide sequence.

ID-124

Clone 3-26

ATGGCAGAAATCACAGCTAAACTTGTAAGAATTGCGTGAAAAATCAGG
TGCAGGCGTTATGGACGCTAAAAAAGCATTAGTAGAACTGATGGTGACC
TTGATAAAGCGATTGAATTACTTCGCGAAAAAGGTATGGCTAAAGCAGCT
AAAAAAGCAGACCGTGTTGCTGCTGAAGGTTTAAACAGGTGTTTATGTTGAT
GGTAACGTTGCAGCAGTTATTGAAGTTAA

MAEITAKLVKELREKSGAGVMDAKKALVETDGDLDKAIELLREKGMAKAAK
KADRVAEGLTGVYVDGNVAIV

Sequence description:

- A) Length: 230 bp - 76 aa (partial sequence)
- B) ATG start codon is preceded by an
typical Shine-Dalgarno sequence. No obvious
potential leader peptide sequence.

FIG. 1^{CONT'D}

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ID-125

Clone 3-33

ATGATAAAAAACCTGTTATTAACAGGTTTTTTATCATTTAATGACGGAAAA
CTGGACACAAATTATTTTCTTGTATAATTAAATATATTATTTCTTATCAGG
AGGTTATGATGACATTAGAGAAACGATTAA

MIKNLLLTGFLSFNDGKLDTNFYFSCHKYIISYQEVMMTLEKRF

Sequence description:

- A] Length: 134 bp - 44 aa (partial sequence)
- B] ATG start codon is preceded by an
typical Shine-Dalgarno sequence. Possible
potential leader peptide sequence.

ID-126

Clone 3-41

ATGAAAAATAATAAAAAATAATGGTTTTCTGAAAAATTCCTTTATTACATA
TTATTGATTATTGCGGTTATTACAACCTTTCAATACTATTAA

MKNNKNNGFLKNSFIYILLIIVITTFQYYL

Sequence description:

- A] Length: 94 bp - 31 aa (partial sequence)
- B] ATG start codon is preceded by a
possible Shine-Dalgarno sequence. Potential
leader peptide sequence.

FIG. 1 CONT'D

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ID-127

Clone 3-42

ATGTTAGATATTATCTTATCCGGAATTCGCAAGGATTACTTTGGTCAATTA
TGGCAATTGGCGTGTTTATCACTTTTCGTATCTTAGACATAGCCGATCTCTC
TGCAGAAGGGGCTTCCCTATGGGGGCTGCAGTTTGCGCCTTATGTATCGT
TAA

MLDIILSGISQGLLWSIMAIGVFITFRILDIADLSAEGAFPMGAAVCAIV

Sequence description:

- A) Length: 158 bp - 52 aa (partial sequence)
- B) ATG start codon is preceded by a possible Shine-Dalgarno sequence. Potential leader peptide sequence.

ID-128

Clone 3-43

ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTTAAATGAG
TATTGATAAACTTAGATATAAAGAACCAGAGAGTGAACATGACAAGCGAC
CTACTTTTTATTGGTAGTACTTATACTTGTTACTGTAGCAGTTATATTGTC
GTTATTAA

MEMPKRNELLNKEIKMSIDKLRYPKEPESEHDKRPTFYLVVLILVTVAVILSLF

Sequence description:

- A) Length: 161 bp - 53 aa (full-length gene)
- B) ATG start codon is preceded by a possible Shine-Dalgarno sequence. Potential

FIG. 1_{CONT'D}

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leader peptide sequence.

ID-129

Clone 3-44

GTGGTAAGTAAATTGAGTTTAAACAACGATTTTTGCATTGCTATTTTCATCA
ATGCTAATTTACGCAACACCTCTTATCTTTACAAGTATTGGGGGAACCTTC
TCTGAACGTGGTGGTATCGTCAACGTTGGTTTAGAAGGAATTATGGTAATT
GGAGCTTTCTCAGGCGTTGTATTAA

MVSKLSLTTIFALLFSSMLIYATPLIFTSIGGTFSEGGIVNVGLEGIMVIGAFSG
VVF

Sequence description:

A] Length: 179 bp - 59 aa (partial sequence)
B] GTG start codon is preceded by a
possible Shine-Dalgarno sequence. Potential
leader peptide sequence.

ID-130

Clone 3-46/47

ATGAGAATTATTGCAATAACTGAAAAGGTTATAAAAGAACTGTTTCGTGAT
AAAAGAACACTTGCTATGATGTTTTAGCACCTATTTAATTATGTTTTGA
TGAATGTTATGTTTTCTGCGAATAGTAATACAAAAGTTAAGATTGGAACCTA
TTAACGTTAACACGAAGGTCGTTTCAAATTTAGATAATATTAAGCATATTC
AAGTGAGATCATTTAAATTTAACTCATCTGCTAAAAAGCACTCAAATCAA
ATAAAATTGATGCTCTTATTTTCGGAGGACAATAAATCTTATACTGTCTTCT
ATGCGAATACAGATTCTTCAAAGACGACTTTAACAAGACAAGCTTTTAAA
ACCGCTGTTAATACAATGAACAGTAAGGAACTGATTTTCGCAAGTTAAATTT
TTAGCTAATAAGAATCCGAACTAGCACAATCCTTACAACTCGCTCCAAA
TATATCAAAGAAAAATATAATTACGGAAATAAAAATACAGGCTTTTTTGC
AAAAATGATACCAATACTAATGGGATTTATGGTCTTCTTCTTGGTTTTT

FIG. 1 CONT'D

47 / 110

MRHIAITEKVIKELFRDKRTLAMMFLAPILIMFLMNVMFSA NSNTKVKIGTINV
NTKVVS NLDNIKHQVRSFKFNSSAKKALKSNKIDALISEDNKS YTVFYANTDS
SKTTLTRQAFKTA VNTMNSKELISQVKILANKNP KLAQSLQTRSKYIKEKYN Y
GNKNTGFFAKMIPILMGFMVFFLVF

Sequence description:

- A] Length: 558 bp - 186 aa (partial sequence)
- B] ATG start codon is preceded by a possible Shine-Dalgarno sequence. Potential leader peptide sequence. C-terminus has yet to be determined.

ID-131

Clone 3-48

GTGATTATCGTTATGAGTAAACATCAAGAAATTTTGGAGTACCTAGAAAAT
TTAGCTGTTGGTAAGAGGGTTAGTGTACGCAGTATTTCAAATCATTAA

MIIVMSKHQEILEYLENLAVGKRVS VRSISNHL

Sequence description:

- A] Length: 100 bp - 33 aa (partial sequence)
- B] GTG start codon is not preceded by a obvious Shine-Dalgarno sequence. No obvious leader peptide sequence.

ID-132

Clone 2-c53

FIG. 1 CONT'D

SUBSTITUTE SHEET (RULE 26)

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ATGTATAGAGAAATTACCGCTGTCGAACACGATCGCTTTGTGAGCGAATCC
AACCAAACAAACCTACTTCAATCTCTTAATTGGCCCAAAGTAAAAGACAA
CTGGGGTAGTCAATTACTTGGCTTTTTTGACGGTGAAACCCAAATTGCCAG
CGCTAGTATTCTCATCAAATCACTTCCTCTTGGCTTCTCCATGCTGTATATT
CCGCGTGGACCAATCATGGATTACTCCAATCTAGATATTGTAAGTAAGGTC
CTTAAGGACCTTAAAGCTTTTGGCAAAAAACAAAGAGCTCTCTTTATCAAG
TGTGATCCTCTCATCTATTT

MYREITAVEHDFVSESNQTNLLQSLNWPVKVDNWGSQLLGFFDGETQIASA
SILIKSLPLGFSMLYIPRGPIMDYSNLDIVTKVLKDLKAFGKKQRALFIKCDPLI
Y

Sequence description:

- A] Length: 326 bp - 108 aa (partial sequence)
B] ATG start codon is preceded by an obvious
Shine-Dalgarno sequence. No obvious leader
peptide sequence.

ID-133

Clone 2-c59

ATGGACAAGAAAAAAATCTTAGTAACGGGTATTGTGCCTAAAGAAGGTCT
AAGAAAGCTTATGGACCGATTTGATGTTACTTATTCAGAAGATCGCCCATT
TTCACGTGACTATGTGTTAGAGCATTTATCTGAATATGACGGATGGTTACT
CATGGGACAAAAAGGTGATAAAGAGATGATTGATGCAGGTGAAAACCTTAC
AAATTATTTCTTT

MDKKKILVTGIVPKEGLRKLMDRFDVTYSEDRPFSRDYVLEHLSEYDGWLLM
GQKGDKEMIDAGENLQIIS

Sequence description:

- A] Length: 215 bp - 71 aa (partial sequence)

FIG. 1_{CONT'D}

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B] ATG start codon is preceded by an obvious Shine-Dalgarno sequence. No obvious leader peptide sequence.

ID-134

Clone 2-c62

ATTTGAAAGATGACTACCAAAATATTAGTTTTGGACAGGATCCAGAAGTT
GTTGATTATGCTGGTCTGTTTGAAAAACGCCGTCCAGTTTTAGAAAAAGCA
GTTAAAAATTTCTTGCAAGAAGAGAGAGCTACGAGAATGCTATCTGATTTC
TTGCAAGAAGAAAAATGGGTAAGTGAATTTGCTGAATTTATGGCGATCAA
AGAATATTTGGTAATAAGGCGCTTCAAGAATGGGATGACAAGGCTATTA
TACGCCGCGAAGAAGAAGCCTTAGCAGGATATCGTCAAAAGCTTAGTGAA
GTGATAAAATATCATGAAGTAACGCAATATTTCTTTTACAAACAATGGTTT
GAGTAAAAAGAATATGCTAATGATAAAGGGATTCAAATTATCGGTGATAT
GCCAATCTACGTTTCTGCCGATAGTGTAAGAAGTTTGGACAATGCCTGAAGT
TTT

ISKDDYQNISFGQDPEVVDYAGLFEKRRPVLEKAVKNFLQEERATRMLSDFLQ
EEKWVTDFAEFMAIKEHFGNKALQEWDDKAIIRREEEALAGYRQKLSEVIKY
HEVTQYFFYKQWFELKEYANDKGIQIIGDMPYVSADSVEVWTMPFLF

A] Length: 459 bp - 153 aa (partial sequence)
B] More sequencing is required to determine the
N- and C-termini
enzyme). - *Streptococcus pneumoniae* (63%)

ID-135

Identical to ID-108 described in WO 00/06736

Clone 2-c63

ID-136

Clone 2-c66

FIG. 1 CONT'D

50 / 110

ATGGCAAAACAGAAAAATAACTGGCGCCGTGTTGGAGTTGGTGTCTTAC
ACTTGCTTCAGTTGCGACTCTTGCTGCATGTGGAAGTAAATCAGCTTCCCA
GGATTCTAATGGAGCGATTAATTGGGCTATTCCAACAGAAATCAATACACT
AGATTTATCTAAAGTTACAGACACTTACTCAAATCTAGCTATTGGTAACTC
TAGTAGTAATTTCTTCGCTTAGATAAAGATGGAAAGACAAGACCAGACTT
GGCTACTAAAGTTGATGTTTCAAAAGATGGCTTAACTTATACAGCTACATT
ACGTAAAGGCTTGAAGTGGTCAGATGGCAGTAACTTACTGCAAAGGATT
TTGTTTATTCATGGCAACGTTTAGTTGATCCTAAAACAGCTTCACAATATG
CTTACCTTGCTGTTGAAGGGCATGTGCTTAATGCCGATAAAATCAACGAAG
GACAAGAGAAAGACTTGAATAAGCTAGGTGTTAAGGCAGAAGGCGATGA
CAAAGTTGTTATTACTTTATCTAGTCCGTCTCCGCAATTCATCTACTACCTT
GCATTCACTAACTTCATGCCACAAAAACAAGAAGTTGTTGAAAAATATGG
AAAAGATTACGCAACTACTTCAAAAAATACAGTTTACTCAGGACCATATA
CTGTTGAAGGTTGGAATGGTTCGAATGGTACTTTACGCTGAAGAAAAAC
AAAAATTATTGGGACGCTAAAAATGTAAAAACAAAAGAAGTTTCGCATCCA
GACTGTTAAAAAACCAGATACCGCCGTTCAAATGTATAAACGTGGTGAGT
TAGATGCAGCTAATATCTCAAATACTTCTGCTATTTATCAAGCTAATAAAA
ATAATAAAGATGTCACAGATGTTCTAGAAGCGACCACTGCCTATATGGAA
TATAATACTACTGGTTCTGTGAAAGGGCTTGATAATGTTAAGATTCTGTCGC
GCCTTAACTTAGCAACTAACCGTAAAGGAGTTGTTCAAGCAGCCGTTGAT
ACAGGCTCAAAACCGGCAATTGCTTTTGCACCTACTGGTTTAGCCAAAACA
CCAGATGGAAGTGAATTTGGCAAAATATGTTGCCCCAGGTTATGAATATAAT
AAAAGTGAAGCAGCAAACTCTTTAGACTA

MAKQKNNWRRVGVGVLTLASVATLAACGSKSASQDSNGAINWAIPTEINTLD
LSKVTDITYSNLAIGNSSSNFLRLDKDGKTRPDLATKVDVSKDGLTYATLRKG
LKWSDGSKLTAKDFVYSWQRLVDPKTASQYAYLAVEGHVLNADKINEGQEK
DLNKLGVKAEGDDKVVITLSSPSPQFIYYLAFTNFMPQKQEVVEKYGKDYAT
TSKNTVYSGPYTVEGWNGSNGTFTLKKNKNYWDAKNVKTKEVRIQTVKKPD
TAVQMYKRGELDAANISNTSAIYQANKNNKDVTDVLEATTAYMEYNTTGSV
KGLDNVKIRRALNLATNRKGVVQAAVDTGSKPAIAFAPTGLAKTPDGTDLAK
YVAPGYEYNKTEAAKLRL

Sequence description:

- A) Length: 1143 bp - 381 aa (partial sequence)
 - B) Shine-Dalgarno sequence precedes ATG codon.
- Possesses a potential leader peptide sequence.

FIG. 1_{CONT'D}

51 / 110

ID-137

Clone 2-c67

TTGAGAGTTTATGAAAATAAAGAAGAGTTGAAAAAAGAAATAAGTAAAAC
ATTTGAGAAATACATTATGGAATTTAATAA
TATTCCAGAGAATCTAAAAGATAAAAAGAATTGATGAAGTTGATAGAACTC
CAGCAGAAAACCTTTCTTATCAGGTTGGCT
GGACCAACTTGGTTCTTAAATGGGAAGAAGATGAAAGAAAGGGACTTCAA
GTAAAAACACCATCGGATAAATTT

MRVYENKEELKKEISKTFEKYIMEFNNIPENLKDKRIDEVDRTPAENLSYQVG
WTNLVLKWEEDERKGLQVKTPSDKF

Sequence description

- A] Length: 234 bp - 78 aa (partial sequence)
- B] TTG start codon is preceded by a potential Shine-Dalgarno sequence. No obvious leader peptide sequence.

ID-138

Clone 2-c70

ATGTCAAAGTTTGATAGTCAGAAAATAATTACTCCGATTATGAAGTTTGTC
AATATGCGAGGGATTATTGCACTCAAAGATGGCATGCTAGCAATTTTACCA
CTAACAGTTGTTGGGAGTCTCTTTTAATATTAGGGCAGCTTCCATT

MSKFDSQKIITPIMKFVNMRGIHALKDGM LAILPLTVVGS LFLILGQLPF

Sequence description

- A] Length: 150 bp - 50 aa (partial sequence)
- B] ATG start codon is preceded by a potential Shine-Dalgarno sequence. Possesses a potential

FIG. 1 CONT'D

52 / 110

leader peptide sequence.

ID-139

Clone 2-c71

GAGACCACTTCATCAGTTAAACCAGCAGGAATTGACCGTATCAATCATACC
TCAACACCCCCGAAGAAAACCTACCCCCAACATTGCAACGACGCATAGCTT
CAAAGATCGTTGTGATACTTTAGAAAGAATTCACAATGAAGACATTGATGT
TTGTTCTGGATTCAATTTGTGGTATGGGAGAGAGCGATGAGGGGCTCATCAC
ATTAGCTTTTCACTAAAAGAACTGAACCCCTATTCTATCCCTGTCAATTTT
TACTTGCTGTTGAAGGAACACCTCTTGAAAATATAACTATTTGACTCCC
ATTAAATGCTTAAAAATTATGGCCATGTTGCGTTTTGTTTTTCCTTTCAAGG
AATTAAGATTAAAGTGCTGGACGGGAGGTCCATTTTGAGAATTTGAATCAT
TAGTCACCTTACTTGTTGACTCAACTTTTTTGGGAAATTACCTAACAGAGG
GGGGTCGCAATCAACATACCGATATTGAATTCTTGAAAAATTACAATA
AATCATACTAAAAAGGAATTAATTT

ETTSSVKPAGIDRINHTSTPPKKTTPNIAATTHSFKDRCDTLERIHNEIDVCSGFI
CGMGESDEGLITLAFRLKELNPYSIPVNFLLAVEGTPLGKYNLYLTPIKCLKIMA
MLRFVFPFKELRLSAGREVFENFESLVTLLVDSTFLGNYLTEGGRNQHTDIEF
LEKLQLNHTKKELI

Sequence description:

A) Length: 535 bp - 178 aa (partial sequence)
B) N- and C-termini require verification

ID-140

Clone 2-c73

ATGCCGGTTTGGACTGCACAGTCTATTCCAAAGGCATTTTTAGAAAAGCAT
AATACTAAGGAAGGCACCTGGGCAAACTAACCATTTCTAAGTGGTTCTTTA
GTATTTTACCAGTTATCTCCTGATGGAGAGGAAATCTCGCGGCATATTTT

FIG. 1 CONT'D

53 / 110

GATGCTAGTAGTGATATTCCTTTTGTGATCCACAAGTCTGGCATAAAGTT
TCGCCGAATAGTCCAGACTTAAGTTGCTATCTAACTTTTTACTGCCAAAAA
GAAGATTACTTCCATAAAAAATATGGTCTCACGCGCACACATTCTGAGGTT
ATCGCCAGTGCACCTCTCTTATCTGAGAAGAGTAATATATTAGACCTTGGG
TGTGGTCAAGGGCGAACTCACTTTATTTATCGCTGCTGGGACATCAAGTG
ACTTCTGTGATTCAAACGGACAGAGCCTTGTAGCTTTAGAAAATATGGCA
TTAGAAGAAGAGCTTCCTTACAATATAAAAAGGTATGATATTAATACTACT
GCTATTGAAGGGCACTATGATTTTATTTTATCAACTGTGGTATTTATGTTTT
T

MPVWTAQSIPKAFLEKHNTKEGTWAKLTILSGSLVIFYQLSPDGEEISRHFIDAS
SDIPFVDPQVWHKVSPNSPDLSCYLTFCQKEDYFHKKYGLTRTHSEVIASAP
LLSEKSNILDGCGQGRNSLYLSLLGHQVTSVDSNGQSLVALENMALEEELPY
NIKRYDINTTAIEGHYDFILSTVVFMF

Sequence description:

- A] Length: 563 bp - 187 aa (partial sequence)
- B] N- and C-termini require verification

ID-141

Clone 2c76

ATGACAAAGCAAATAATTGCCATTTGGGCTGAAGATGAAGACCATTTGAT
TGGAGTTAATGGCGGTTTACCATGGAGGCTTCCTAAAGAGTTACATCACTT
CAAAGAAACGACCATGGGGCAGGCTTTGCTTATGGGACGAAAGACCTTTG
ATGGAATGAACCGTCGTGTTTTACCTGGTAGAGAGACAATCATCTTAACAA
AAGATGAACAATTCCAAGCAGATGGAGTGACAGTCCTAAATAGTGTGAA
CAAGTTATAAAATGGTTTCAGGAACATAATAAGACCTTATTTATTGTAGGT
GGTGCAAGTATTTATAAAGCATTTCTGCCTTATTGTGAAGCAATCATAAAA
ACTAAAGTTCATGGAAAATTCAAAGGTGATACCTATTTTCCTGATGTTAAT
CTATCTGAGTTT

MTKQIIAIWAEDEDHLIGVNGGLPWRLPKELHHFKETTMGQALLMGRKTFDG
MNRRLVLPGRETIILTKDEQFQADGVTVLNSVEQVIKWFQEHNTLFIIVGGASI
YKAFLPYCEAIKTKVHGKFKGDTYFPDVLSEF

FIG. 1 CONT'D

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Sequence description:

- A] Length: 417 bp - 139 aa (partial sequence)
B] ATG start codon is preceded by a Shine-Dalgarno sequence. No leader peptide sequence

ID-142

Clone 2-c78

TTGTGGCCAACTGTGCCCCGCTTATTAATAGCACTTTGTTACCAATTGAA
GATATCTTAACATCAGGTGCTCATAGCAACCCTATTTTAATGGGGGTTATA
CTTGGCGGGACAATTGTAGTAGTGGCGACAGCACCCTTTCTTCTATGGCA
TTGACAGCTATGCTAGGATTAACCGGAATGCCTATGGCTATAGGAGCCTTG
TCTGTCTTTGGTTCGTCAATTTATGAATGGTGTACTTTCCATAAATTTAAAC
TTGGAAGTCGTAAAGATAATATAGCTTTTGCTGTTGAGCCTCTAACTCAAG
CTGACGTGACTTCAGCTAACCCTATTCCAATCTATGTCACTAATTTTGTGG
TGGTGCAGCTTGTGGTATTTTAATTGCCTTGATGAAATTAGTTAATGATACT
CCTGGAACAGCGACACCAATTGCAGGATTTGCTGTCATGTTTGCCTATAAC
CCAATGATAAAAGTACTAATAACCGCTCTAGGTTGTATTATCCTATCTTTA
CTAGCAGGCTATTTTGGAGGCATTGTTTTT

MWPNCAPLINSTLFTIEDILTSGAHSNPILMGVILGGTIVVVATAPLSSMALTA
MLGLTGMPMAIGALSVFGSSFMNGVLFHKLKLGSRKDNIAFAVEPLTQADVT
SANPIPIYVTNFVGGAAACGILIALMKLVNDTPGTATPIAGFAVMFAYNPMIKVL
ITALGCIILSLLAGYFGGIVF

Sequence description:

- A] Length: 540 bp - 180 aa (partial sequence)
B] N- and C-termini have yet to be elucidated

ID-143

FIG. 1_{CONT'D}

55 / 110

Clone 2-c80

ATGTTTTTAAGTATAATGGCAGGTGTCATAGCATTGTCTGACAGTTATT
GCCATTCCACGCTTCATTAAGTTTTACCAATTGAAGAAAATTGGCGGGCAA
CAAATGCATGAAGATGTCAAACAACATCTAGCCAAAGCAGGTACGCCGAC
AATGGGAGGAACGGTATTTT

MFLSIMAGVIAFVLTVIAIPRFIKFYQLKKIGGQQMHEDVKQHLAKAGTPTMG
GTVF

Sequence description:

- A] Length: 172 bp - 57 aa (partial sequence)
- B] Shine Dalgarno sequence precedes 'ATG' start codon. Possesses a potential leader peptide sequence.

ID-144

Clone 3-83

ATGAAACCATATTTATCTTTTATTGGTAGAACGTTATTATACTTCGGTATTT
TATTGTTACTAATTTACTTTTTGCATACCTTGGTCGCGGACAAGGCAGTTT
TATTTATAA

MKPYLSFIGRTLTYFGILLLLIYFFAYLGRGQGSFIY

Sequence description:

- A] Length: 113 bp - 37 aa (partial sequence)
- B] Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a potential leader peptide sequence.
This orf is not in frame with nuc

FIG. 1 CONT'D

56 / 110

ID-145

Clone 3-86

ATGTCATATTTTAGAAATTACTGGTATCGTTTTGGAGCAATTTTATTTATTA
TTTAGCAGTAATATTGCTTGTTTTAGACCTGACTGGTCAATGCTTCACTA
TCTATTGTATTTTACTTTATGGCACTTCTAGCGCATCAATTTGAAGAATAT
CAGTTTCCCGGTGGGGCATCACCTATCATTAACTATGTTGTTTATGATGAA
GAAGAGCTGATGGATTGTTTTCCAGGCAATACTCAGTCTATTATGTTGGTT
AATACTATTGCTTGGTTGCTTTACATTGCTAGTATTGCTTTTCCTCAAGCTT
ATTGGCTTGGATTAGGAGTCATGTTCTTTAGTCTAACGCAGCTCTTGGGTC
ATGGTTTTCAGATGAATATTAAACTTAAACTTGGTATAATCCTGGTCTAG
CAACGACAGTATTTCTCCTAGTACCAATAGCTTGCGCATACATCTATCAAG
CTAGTGCAGAAGGAATGCTCACTTGGGGAGATTGGCTAGGTGGTTTTATCA
TGTTGATTGTCTGTGTACTAACTAGCATTATTGCACCTGTACAGCTATTGAA
GGATAAGGAGACCAATTATATTATTAGTCCTTGGCAAATGGACCGTTTTCA
TAAGGTCGTTAATTTTGTAAAGGATAAAAAAATAA

MSYFRNYWYRFGAILFIILAVILLVFRPDWSMLHYLLYFYFMALLAHQFEEYQ
FPGGASPIINYVVYDEEELMDCFPGNTQSIMLVNTIAWLLYIASIAFPQAYWLG
LGVMFFSLTQLLGHGFQMNILKLTWYNPGLATTVFLVPIACAYIQASAEG
MLTWGDWLGGFIMLIVCVLTSIIAPVQLLKDKETNYIISPWQMDRFHKVVNFV
RIKK*

Sequence description:

- A] Length: 651 bp - 219 aa (full length gene)
- B] Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a potential leader peptide sequence.

ID-146

Clone 3-c88

FIG. 1_{CONT'D}

57 / 110

ATGCCACTTACAGCACTTGAAATTAAAGATAAAACATTTTCATCAAAATTT
CGCGGTTATAGCGAAGAAGAAGTT

MPLTALEIKDKTFSSKFRGYSEEEV

Sequence description:

- A) Length: 75 bp - 25 aa (partial sequence)
- B) Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. No leader peptide

ID-147

Clone 3-90

ATGTCACCTTTTTCAAGAAAAAATTGCTTACAATTGCGCTAAAAAGGAAGCG
CTTTATAAAGAGAGTTTAGGACGCTACGCCTTGAGATCAATGCTAGCAGG
GGCTTATTTGACAATGAGTACTGCTGCCGGTATCGTCGCAGCTGATACTAT
TGGTAAAATTTCTCCTGCTCTATCAGGTTTTGTATTTGCTTTCATCTTTAGTT
TTGGACTTATTTATGTTTTAATATTTAATGGTGAATTGGCGACATCTAATAT
GCTTTATCTCACTGCAGGAGCCTATAATAAAAAATATCTCTTGAAAAAAGC
CATAACAATTTTAATTTATTGTACTTTTTTCAACCTCGTTGGTGCTTGTATA
TTAGCTTGGTTGTTTAA

MSLFQEKIAYNCAKKEALYKESLGRYALRSMLAGAYLTMSTAAGIVAADTIG
KISPALSGFVFAFIFSFLIYVLIFNGELATSNMLYLTAGAYNKNISWKKAITILI
YCTFFNLVGACILAWLF

Sequence description

- A) Length: 406 bp - 125 aa (partial sequence)
- B) Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possible leader peptide

FIG. 1 CONT'D

58 / 110

ID-148

Clone 3-92

AAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAACCAGCTTC
AACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCAACCTC
ATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAA
TTCAGTACATAACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGC
AGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGTTGCACA
GTACTCTACACAAAATATGGCAGCAAATAACATTTTCATATGTTATCTGGCA
ACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCTAATACTTG
GAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCCTATGACCACGT
TCACGTATCATTTAA

KLQATEVKSVPVPAQPASTTNAAHPENAGLQPHVAAAYKEKVASTYGVNEF
STYRAGDPGDHKGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQ
KFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVVSF

Sequence description

- A] Length: 419 bp - 139 aa (partial sequence)
B] N- and C-termini have yet to be determined

ID-149

Clone 3-94

ATGATTCCAGTAGTTATTGAACAAACAAGTCGTGGTGAACGTTCTTATGAT
ATTTACTCACGTCTTTTAAAAGATCGTATTATTATGTTGACAGGCCAAGTT
GAGGATAATATGGCCAATAGTATCATTGCACAGTTATTGTTTCTCGATGCA
CAAGATAATACAAAGGATATTTACCTTTATGTCAATACACCAGGTGGTTCA
GTATCGGCTGGACTTGCTATTGTGGACACCATGAACTTCATTAAATCGGAC
GTACAGACGATTGTTATGGGGATGGCTGCTTCGATGGGAACCATTATTGCT
TCAAGTGGTGCTAAAGGAAAACGTTTTATGTTACCGAATGCAGAATATATG

FIG. 1 CONT'D

59 / 110

ATCCACCAACCAATGGGCGGAACAGGCGGAGGTACACAGCAATCTGATAT
GGCTATCGCTGCTGAGCATCTTTTAAAAACGCGTCATACTTTAGAAAAAAT
CTTAGCTGATAATTCTGGTCAATCTATTGAAAAAGTCCATGATGATGCAGA
GCGTGATCGTTGGATGAGTGCTCAAGAACTTGATTATGGCTTTATTGAT
GCTATTATGGAAAAATAATAATTTACAATAATAGATTAAAAAGAGTTGAGTT
TACCAACTCTTTTTTTATTGTTGGAATTATGTTATAATCTTAGTAATTACA
GATATGACGCAGAAAGGAAAAAATTATTGA

MIPVVIEQTSRGERSYDIYSRLLKDRIIMLTGQVEDNMANSIIAQLLFLDAQDN
TKDIYLYVNTPGGSVSAGLAIVDTMNFIKSDVQTIVMGMAASMGTHIASSGAK
GKRFMLPNAEYMIHQPMGGTGGGTQQSDMAIAAEHLLKTRHTLEKILADNSG
QSIEKVHDDAERDRWMSAQEHLIMALLMLLWKIIYNNRFKRVEFTNSFFICW
NYVILVITDMTQKGKNY*

Sequence description

- A] Length: 693 bp - 231 aa (full length gene)
B] Putative ATG start codon is preceded by a
typical Shine-Dalgarno sequence. No leader
peptide. Significantly, it would appear to have a
very hydrophobic C-terminus.

ID-150

Clone 2-c86

ATGAAACCAAAAATTATTGGTGTACTTGGTCTAGGAATATTTGGACAAACA
CTCGACAAGAAGTAAGTAAGTCTTTGAACAAGATGTTATTGCTATTGACAGC
AATCCTGAAAATGTACAAGCTGTCGCCGAAGT
TGTTACAAAAGCAGCTATCGGAGACATTACTGATTTAGCTTTCCTAAAAACA
CATCGGGATCAGTGACTGTGATACTGTTATTATTGCTACAGGAAACAGTTT
AGAGAGCTCAGTATTGGCCGTAATGCACTGTAAAAAGTTAGGCGTCCCAC
AAGTTATTGCTAAAGCTCGAAACCTTGATACGAAGAAGTACTTTATGAAA
TTGGTGCTGATTTGGTTATCTCTCCGGAGCGAGAATCTGGGCAAAATGTTG
CTGCAACCTCATGAGAAATAAAATTACAGATGTCTTCCAGATTGAATCTG
ATATTTCTGTCATTGAATTT

MKPKIIGVLGLGIFGQTLAQELSNFEQDVIAIDSNPENVAEAVVTKAAIGDI
TDLAFLKHIGISDCDTVIIATGNSLE

FIG. 1 CONT'D

60 / 110

SSVLAVMHCKKLGVPQVIKARNLVYEEVLYEIGADLVISPERESGQNVAAN
LMRNKITDVFQIESDISVIEF

Sequence description:

A) Length: 459 bp - 153 aa (partial sequence)
B) Putative ATG start codon is preceded by a
typical Shine-Dalgarno sequence. Possesses a
potential leader peptide sequence.
This orf is not in frame with nuc

ID-151

Clone 2-c88

GTGCGTTATAGTAAAGAGATTATTCAGTTAGCTATACCAGCTATGATTGAA
AATATCTTACAAATGCTCATGGGAGTAGTTGATAATTATCTAGTGGCTCAG
TTAGGTGTTGTAGCAGTATCAGGTGTTTCAGTTGCTAATAATATAATTACT
ATTTATCAAGCTATTTTTATAGCTTTAGGGGCGAGTATAGCAAGTCTATTG
GCCAAGTCGTTAGCAGGTAGTGAGAAGGATGATGCAATTTTCAGTATGTTCT
CAAGCCATTTTCTAACATCACTGATAGGGGCAGTATTAGGAATTATCTCG
ATTGTTTTTGGACAAACTTTCTTT

MRYSKHEIQLAIPAMIENILQMLMGVVDNYLVAQLGVVAVSGVSVANNIITY
QAIFIALGASIASLLAKSLAGSEKDDAISVCSQAIFLTSLIGAVLGIISIVFGQTFF

Sequence description

A) Length: 330 bp - 110 aa (partial sequence)
B) Putative GTG start codon is preceded by a
typical Shine-Dalgarno sequence. May have a
leader peptide

ID-152

FIG. 1 CONT'D

61 / 110

Clone 2-c92

TTGATTAACAAGTATTCGTGCTTTTTGAAGAGGATTCTCCATAATAATACT
CCTTTAATAGTTATCGTGAGAAGTATTTTAAAGAAAAACCGCCAAGGTAG
AGCGACATTTCTGCCTTTAACTACAATAAAACCAAGAGAATTAGCACAAAC
ATTATCTCTCAAAATTACAAAGTTCTCAAGGGTTTTAGGAATAGCTAGTG
AATTGGTAACCTATGATCAACGCTTGTCAAACATTTTT

MINKYSCFLKRILHNNTPLIVIVRSILKKNRQGRATFLPLTTIKPRELAQHLYSK
LQSSQGFLGIASELVTYDQRLSNIF

Sequence description

A] Length: 240 bp - 80 aa (partial sequence)

B] No obvious Shine Dalgarno sequence precedes the Putative TTG start
codon

ID-153

Clone 2-c94

TTGTTGACTCACAAAAATATATTATTAACCATTATATTTGGATTATTTATGA
TTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATA
ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAAT
ACTTTTGTTCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTG
ATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTGAAAT
GGCAGCCTATTAAGTGGGATATGAAAGAACTGAACTTAATAATGGTAAT
ATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAA
AGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAA
AACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAG
GAGCCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAACGCTAAACCTGATA
TTTTAAAAAAGTTTGTAAGGAAAAGAAGCAGTTCAATACGATACTTTC
ACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATT
GATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAA

FIG. 1 CONT'D

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MLTHKNILLTIIFGLFMIILSACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFV
PMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKETELNNGNIDLI
WNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQSG
SSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANY
YLKQEG

Sequence description

A] Length: 649 bp - 216 aa (partial sequence)
B] TTG start codon is preceded by a possible
typical Shine-Dalgarno sequence. Has a
leader peptide

ID-154

Clone 2-c100

ATGAAAATTTGGAAAAAATAACCTTAATGTTTTCTGCAATTATTTTAACA
ACAGTAATTGCATTGGGAGTCTATGTTGCCTCAGCTTATAATTTTCGACTA
ATGAATTGTCTAAGACTTTT

MKIWKKITLMFSAILTTVIALGVYVASAYNFSTNELSKTF

Sequence description

A] Length: 123 bp - 41 aa (partial sequence)
B] ATG start codon is preceded by a potential
typical Shine-Dalgarno sequence. Has a
typical leader peptide

ID-155

Clone 2-c1

FIG. 1_{CONT'D}

63 / 110

ATGAAAAAACAAGACTATTACTGCTTTTTGGAGGCTTATTAATAATGATA
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA
GGAATACCAGGCAGAACAGAAATTTTAAGTCATACTTTAAATATATATCAG
ATAAAAATAACTATTTAGATAATATAAAAGTTTATTACTTTTCTATAAGTA
TTTCTAAAGATGTACAAGATAAAGTCAGTGAAACAACAACCTTGTTTCATATA
GACTAGAAAAGCAAAAGAATCAAGAGTTCATTGGTAATTTTGAACATGAA
GTTAGTGAATCTAGTCAATATTCAACCGAAGTTAAAAATCAAATACAGTAT
CCAATCCAGTATAAAGATAATTCAATTCGTTTTACTGAAAAACACCGTCA
GAACGTTATGATGAGTTTGTITTTAGTTCATTTGATTCTTCATTATTA
AATATAAAATATATGATTACTTACTAAAACATCCCGAAACTGAATTA
GGTGTTCCTATAAGATTCCTATAAATTCTGAAATTGTAGCCCCCTTTATAA
ATCAATTAATATAAAAAATCCTAAAAAATCATCTATTTTCGTTACAAAAA
CGGAAAGTAAAGAATATTATTATACAATCAGTATTGATACTGATTCTGAGA
TATATTCTATATTCGAAGGTATTCAT

MKKQRLLLLFGGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYFKYISDKN
NYLDNIKVVYFISISISKDVQDKVSETTTCYSRLEKQKNQEFIGNFEHEVSESSQ
YSTEVKNQIQYPIQYKDNSIRFTEKTPSERYDEFVSSFDSSLKKYKIYDYLLK
HPETELKGVSYKIPINSEIVAPFINQLNIKNPCKSSISVTKTESKEYYYTISIDTDS
EIYSIFEGIH

Sequence description

- A] Length: 687 bp - 229 aa (partial sequence)
- B] ATG start codon is preceded by a potential typical Shine-Dalgarno sequence. Has a typical leader peptide. C-terminus has yet to be verified

ID-156

Clone 2-c5

ATGACATTTGACACCATTGATCAATTAGCGGTTAATACAGTCCGCACGCTT
TCTATTGATGCTATCCAAGCAGCAAATTCTGGGCACCCAGGTCTTCCTATG
GGAGCTGCGCCTATGGCTTATGTGCTTTGGAATAAATTCTTAAATGTAAAC
CCAAAAACAAGTCGCAATTGGACAAACCGTGACCGTTTTGTACTTTCAGCT

FIG. 1 CONT'D

64 / 110

GGGCATGGTTCAGCTCTTCTTTATAGCCTACTTCATTTAGCTGGCTATGATT
TATCAATTGATGATTT

MTFDTIDQLAVNTVRTLSDAIQAANS GHPGLPMGAAPMAYVLWNKFLNVNP
KTSRNWTNRDRFVLSAGHGSALLYSLHLAGYDLSIDD

Sequence description

A] Length: 272 bp - 90 aa (partial sequence)
B] ATG start codon is preceded by a potential
typical Shine-Dalgarno sequence. No obvious
leader peptide

ID-157

Clone 2-c8

ATGAGAACACTATTTAGAATGATATTTGCTATTCCAAAGTTTATCTTTAGA
TTGATTTGGAATATCATTTGGGGAATATTCAAGACAGTTCTTGTTATTGCG
ATTATTTTATTTGGCTTGTATTACTATGCGAATCACAGTCAATCAGAATTTG
CTAATCAACTTAGTGACATTATTCAGACAGGAAAAACATTTTT

MRTLFRMIFAIPKFIFRLIWNIIWGIFKTVLVIAIILFGLYYYANHSQSEFANQLS
DIIQTGKTF

Sequence description

A] Length: 197 bp - 65 aa (partial sequence)
B] ATG start codon is preceded by a potential
typical Shine-Dalgarno sequence. Possesses a
leader peptide

ID-158

FIG. 1 CONT'D

65 / 110

Clone 2-c9

ATGTCAAAAAAAAAATAATATTAGGAATTTTATCTCTTTTATCTGTCGTTACTT
TGGTGGCGTGTGGTTCATCAGACAAACAGCTACAAGATAAAGTTGAGAAA
AAAGGGAAGTTAGTTTTAGCGGTGAGTCCAGATTATGCTCCCTTTGAGTTT
MSKKIILGILSLLSVVTLVACGSSDKQLQDKVEKKGKLVLA VSPDYAPFEF

Sequence description

A] Length: 153 bp - 51 aa (partial sequence)
B] ATG start codon is preceded by a potential
typical Shine-Dalgarno sequence. Possesses a
leader peptide (not in frame with nuc)

ID-159

Clone 2-c10

ATGAAAAATCAAAGACTATTACTGCTTTTTGGAGGCTTATTAATAATGATA
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA
GGAATACCAGGCAGAACAGAATTTTAAGTCATACTTT
MKNQRLLLLFGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYF

Sequence description

A] Length: 139 bp - 46 aa (partial sequence)
B] ATG start codon is preceded by a potential
typical Shine-Dalgarno sequence. Possesses a
leader peptide

FIG. 1^{CONT'D}

66 / 110

ID-160

Clone 2-c11

ATGATTGGAAAATTATATTATAGCTATAGAAAGTCACGCTTATTAAGAAGT
ATTTTATGGCTTATTTTAATTGTTGGTGTATATATGTTAGGACAACGTGTTT
TATTATCCACTGTTCCCTTATCACATCAAGAGATAAACTAGCAGTAGATC
AACATTTACTCAATAACTTTTCAGCAGTAAGTGGTGGGAGTTTTAATAAAT
TAAATGTTTTCACACTGGGGTTGAGTCCATGGATGTCAAGTATGATTATTT
GGAGATTCGTTTCCTTATTTTCGTGGGCAAAAAATGCAACGAAGCGAAAA
GCAGAAGTAGCTCAATATACTTTAATGCTTACTATCTCAGTTATACAAGCA
TATGGTGTTCAGGAAATCAATTTATAAAAAGCTCTTTATTAGGTTCTTATA
GTGATATTGTTTTT

MIGKLYYSYRKSRLRSILWLILIVGVYMLGQRVLLSTVPLSHQEIKLAVDQHL
LNNFSAVSGGSFNKLNVTGLSPWMSSMIIWRFVSLFSWAKNATKRKAeva
QYTLMLTISVIQAYGVSGNQFIKSSLLGSYSdivF

Sequence description

- A] Length: 423 bp - 141 aa (partial sequence)
- B] ATG start codon is preceded by a potential
typical Shine-Dalgarno sequence. Possesses a
leader peptide

ID-161

Clone 2-c13

ATGAAAGGTCTATTGGATTTTTTAGTTAATATTGCCAGAACGCCAGCTATT
TTAGTCGCCTTGATAGCCATTATCGGTTTAGTACTGCAGAAAAAAGGTGTT
CCTGATATTGTAAAAGGTGGAATAAAAACATTTGTTGGCTTCTTAGTGGTT
TCTGAAGGTGCAGGGATAGTCCAAAATTCCTTGAATCCATTTGGAAAAATG
TTTGAACATGCTTTTCATTTGGTGGGGGTAGTTCCTAATAATGAAGCCATT
GTAGCAGTAGCTCTTACGAAGTATGGCTCAGCAACTGCTTTGATTATGTTA
GCGGGAATGATTTTTAATATTTTAATTGCTCGTTTTACAAAA

FIG. 1 CONT'D

67 / 110

MKGLLDFLVNIARTPAILVALIAIIGLVLQKKGVDPDIVKGGIKTFVGFLVVSEG
AGIVQNSLNPFGKMFHAFHLVGVPNPNEAIVAVALTKYGSATALIMLAGMI
FNILIAFTK

Sequence description

A] Length: 348 bp - 116 aa (partial sequence)
B] ATG start codon is preceded by a potential
Shine-Dalgarno sequence. Possible leader
peptide

ID-162

Clone 2-c21

TTGGTTGGTAAGCCCCAATTACTATTTTTAGATGAACCTACTTCCGGAATG
GATACTTCCACACGTCAACGATTTTGGAGCTGGTTGCGACACTAAAAAA
AGAAGGTGACACAATTGTCTATTCTAGTCATTATATCGAAGAGGTAGAAC
ATACAGCTGATAGGATTTTAGTACTTCATAAAGGAAAGTTATTACGCGATA
CAACCCCTTTGCCATGAAGCAAGAAAAAACCAGAAAGTTATTACCGTT
CCGCTTAGTTATCAAAAATTATTACCTACCTATTTGATTACAGAGTGTGAA
GCCAAGAGTGATAGTATAACGTTTGTACTGGGGAGGCTGAAACTGTATG
GAAAATACTGGCAGATAATGGTTGTCCTATTGAAGCTATTGAGATGACCA
ATAGAACTTTGTTAAATCGTATTTTTGAGACTACTAAGGAGGTAAAACATG
AGAATCTTTA

MVGKPQLLFLDEPTSGMDTSTRQRFWKL VATLKKEGDTIVYSSHYIEEVEHTA
DRILVLHKGKLLRDTPFAMKQEKTEKLFTVPLSYQKLLPTYLITECEAKSDSI
TFVTGEAETVWKILADNGCPIEAIEMTNRTLNRIFETTKEVKHENL

Sequence description

A] Length: 462 bp - 155 aa (partial sequence)
B] Putative TTG start codon is not preceded by
an obvious Shine-Dalgarno sequence. No obvious
leader peptide. N- and C- termini require further

FIG. 1 CONT'D

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examination.

ID-163

Clone 2-c25

TTGAAAAAATCCAAGAGAAGCCGTAAGGCAGTGACAACAAGTGGTGAGA
AGACTTTACTTGAGGATTTGGCAAAAATGAATTTCTAGACGAAGTCATTA
ATGTTATGGTTTTATATACCTTGAATAAGACAAAATCTGCTAACTTAAATA
AGGCCTATATCATGAAAGTTGCTAATGATTTTGCCTTTCAGAATGTTATGA
CGGCCGAAGATGCTGTGCTTAAAATTCGTGATTTTTCAGATCAAAAAGTAA
GGACTAAACAGAAACGAAGAAGAAACAATCGAATGTTCTGAATGGAGT
AATCCTGATTATAAAGATGAGGTTAGCCCAGAAAAAGAAATTGAATTAGA
ACAGTTT

MKKSKRSRKAVTTSGEKTLLEDLAKMNFLDEVINVMVLYTLNKTKSANLNK
AYIMKVANDFAFQNVMTAEDAVLKIRDFSDQKVRTKTETKKKQSNVPEWSN
PDYKDEVSPKEIELEQF

Sequence description

- A] Length:360 bp - 120 aa (partial sequence)
- B] N- and C- termini require verification.

ID-164

Clone 2-c28

ATGACGAATCATATTACTAAACTGATAGAAAATAGCGGAAAAAAATTGAC
AGAAATTAGCGAAGCTACAGATATAGCCTATCCTACACTTTCTGGATACAA
TCAAGGAATCCGCAAACCTAAAAAAGATAATGCTGAAAAATTGGCAAAAT
ACTTTAATGTTTCCGTCGCTTACATTATGGGACTTGATAGCAACCCACATG
CTCCATCAAATCTT

MTNHITKLIENSGKKLTEISEATDIAYP T LSGYNQGIRKPKKDNAEKLAKYFNV
SVAYIMGLDSNP HAPS NL

FIG. 1_{CONT'D}

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Sequence description

- A) Length: 218 bp - 72 aa (partial sequence)
B) ATG start codon is preceded by an obvious Shine Dalgarno sequence. No obvious leader peptide.

ID-165

Clone 2-c29

TTGATGAAAAGGAATAAACATTTACCGTTAACAGAACTACCTATTATATT
TTATTAGCTTTGTTTGAGGAAGCGCATGGCTATGCTATTATGAAAAAAGTT
GAAGAAATGAGTGGCGGTGATGTTAGAATAGCCGCAGGGACAATGTACGG
TGCCATTGAAAATTTACTTAAACAAAAATGGATAAAGTCTATCTCAAGTGA
CGATAGAAGAAGAAAAGTTTATATTATTACTGAGACAGGAAAAGAAATAG
TAGAACTTGAAACGAATCGATTAAGAAAGTTACTTAATACTGCTAATCAGT
TGGGTTTTGGAGGAGATGGTTATGATAAAGTTT

MMKRNKHLPLTETTTYILLALFEEAHGYAIMKKVEEMSGGDVRIAAGTMYG
AIENLLKQKWIKSISSDDRRRKVYIITETGKEIVELETNRLRKLLNTANQLGFG
GDGYDKV

Sequence description

- A) Length: 337 bp - 112 aa (partial sequence)
B) TTG start codon is preceded by an obvious Shine Dalgarno sequence. Actual start codon may ATG that comes immediately after the TTG. Potential leader peptide.

ID-166

FIG. 1_{CONT'D}

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Clone 2-c35

CCCATTACTGGTGAGTTAATAGCTGAGAAATTAGGAGTACCAAGAGCAGC
ACTAAGGTCTGATTTGCGGGTTTTAAGTATGCTAGGTATCATAGATGCAAA
ACCTAAGGTTGGTTATTTTTATTTAGGACAGTATCATGCTTCAATAGGGAC
AAGTCATTTTGAAAAGATGACAGTTTCAGAAATTATGGGGATCCTTCTGAC
AGTTCATCAAAAAGATTCAGTTTATGATGTTATTGTACATATTTTTATGGA
AGATGCTGGTTGTGCTTTTATCTTGGATGATGATGATTTTCTCTGTGGAGTC
GTGTCACGTAAAGATTTACTAAAAACCAGTATTGGCGGAGGAGATCTTTCT
AAAATGCCAATAGGAATGGTGATGACACGTATGCCACACGTGACAACTGT
TTTAGAAAATGAAAGTCTTTTTGCGGCAGCTGATAAATTAGTGAGCAGAA
AAGTGGATAGTCTCCCTGTCGTTTCGTCATGATAAGCAATATCCCGAAAAAT
TTA

PITGELIAEKLGVPRALRSDLRLVLSMLGIIDAKPKVGYFYLGQYHASIGTSHF
EKMTVSEIMGILLTVHQKDSVYDVIVHIFMEDAGCAFILDDDDFLCGVVSRKD
LLKTSIGGGDLSKMPIGMVMTRMPHVTTVLENESLFAAADKLVSARKVDSL PV
VRHDKQYPEKF

Sequence description

A] Length:511 bp - 170 aa (partial sequence)

B] N- and C-termini to be determined

ID-167

Clone 2-44

TTGGAAGTCATCATGCAATTTATTTATAGTATTATTGGTATTTTATTGGTAT
TAGGAATTGTGTATGCAATTTCTTTCAATCGTAAGAGTGTTTCTCTAAGTTT
AATTGGAAAAGCTCTTATCGTTCAATTCATTATTGCGCTAATCTTAGTACGT
ATCCCACTAGGCCAACAAGTTGTTAGTGTTGTTTCAACTGGAGTTACTAAA
GTAATCAACTGTGGTCAAGCTGGTTT

MEVIMQFIYSIIGILLVLGIVYAISFNRSVSLSLIGKALIVQFIILILVRIPLGQQ
VVSVVSTGVTKVINCGQAG

FIG. 1 CONT'D

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Sequence description

- A) Length:233 bp - 77 aa (partial sequence)
B) TTG start codon is preceded by a possible Shine Dalgarno sequence. Actual start codon may occur further downstream. Potential leader peptide.

ID-168

Clone 2-46

CAACCTAATAAAGCTTTAGAAAGTGATGAGATTGATATTAATGCTTTCCAG
CATTATAATTACTTAACCAATTGGAATAAAGCAAATAAGACCAATCTTGTT
TCCGTTGCTGAGACATACTTTACTTCCTTTAGATTATACTCTGGTACTAAGA
ACGGTAAAGGTAAATACCAAACAGTTTCTGAAATTCCAAATAAAGCAACT
ATTACTATCCCAAACGATGCAGTTAACGAAAGTCGCTCTCTCTACTTGTTA
CAATCAGCAGGCTTGCTAAAATTGAAAGTATCAGGTGATACATTAGCAAC
AATGTCAGATGTTGTTTCCAATCCTAAATCTTTAGATT

QPNKALESDEIDINAFQHYNLYTNWNKANKTNLVSVAETYFTSFRLYSGTKN
KGGKYQTVSEIPNKATITIPNDVNESRSLYLLQSAGLLKLKVSGDTLATMSD
VVSNPKSLD

Sequence description

- A) Length:344 bp - 114 aa (partial sequence)
B) N- and C- termini require verification

ID-169

Clone 2-47

ATGAAATGTATAATAAATAATATAAATAAAATAAAAATGATAATTGAGAT
TTATCATAGAAGGAAAACATTTTGAAATTAAATAAAAATCATATTATCTAC

FIG. 1_{CONT'D}

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TGCAGCTCTTACTGCTCTCTTTTTAGGATATAATAGCGTTACTGCGGATACA
TATAATAACTATCAGCCACATAGATCAAATAATATGGATTTAAGTGA
ATATAACTATAATAACCAGATAGAACTTCAGGAGCGTATAAAAAACCTAA
ATATACCTTTT

MKCIINNINKIKMIIIEIYHRRKTILKLNKIILSTAALTALFLGYNSVTADTYNNY
QPHRSNNMDLTEEYNYNQIELQERIKNLNIPF

Sequence description

- A] Length:264 bp - 88 aa (partial sequence)
- B] There is a Shine-Dalgarno sequence upstream of this sequence. Potential leader peptide sequence

ID-169

Clone 2-47

ATGAAATGTATAATAAATAATATAAATAAAATAAAAATGATAATTGAGAT
TTATCATAGAAGGAAAACCTATTTTGAAATTAAATAAAATCATATTATCTAC
TGCAGCTCTTACTGCTCTCTTTTTAGGATATAATAGCGTTACTGCGGATACA
TATAATAACTATCAGCCACATAGATCAAATAATATGGATTTAAGTGA
ATATAACTATAATAACCAGATAGAACTTCAGGAGCGTATAAAAAACCTAA
ATATACCTTTT

MKCIINNINKIKMIIIEIYHRRKTILKLNKIILSTAALTALFLGYNSVTADTYNNY
QPHRSNNMDLTEEYNYNQIELQERIKNLNIPF

Sequence description

- A] Length:264 bp - 88 aa (partial sequence)
- B] There is a Shine-Dalgarno sequence upstream of this sequence. Potential leader peptide sequence

FIG. 1_{CONT'D}

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ID-170

Clone RS-58b

TTGGGTGATTATTATGGTAAGAAATATTTTGGTGAGGCAGCTAAAAAAGA
CGTCGAACATATGGCTAAGAAAATCATTAAATGTCTATAAAACACGGTTAA
AAAACAACACTTGGTTATC
AGAAAATACAAAAGCAATGGCCATTAAGAACTTGATAACATGAGATTAA
TGATTGGCTATCCAGAAGATTATCCTGATCTTTATCGTCAGTACCAATTTG
ATAGTAAAGCAAGCTTCTTTGAAAACAATGATAACTACAGAAAATTATCG
AACAAGAAAACATTTGAAGAATTTAACCAGTCTAATCAACGTGAACATTG
GCAAATGAGTGCCAATGCTGTAAATGCTTATAATGATCCTAATACCAATTC
CATAGTCTTTCCAGCAGCGATTTTTCAATCACCAGTACGATAAACTAA
AACAGTTAGTCAAAATTATGGAGCTATCGGAGCAATTATTGGTCATGAAAT
TTCACACTCATTTGATATTAATGGTATGAAATATGACGAGAAAGGGAATCT
TCACGATTGGTGGACTAAAGAAGATTTAAATCATTATAAGAAATCAACAC
AAGCTATGATTGACCAATGGGATGGCCTTAAAGCAGATGGCGGTAAAGTT
GATGGTAAATTAACCTTTAGCAGAAAATATTGCAGATAATGGTGGTGTTATG
GCATCTCTAGAAGCTCTTAAGACTGAAAAAATCCAACTATAAAGAATTTT
TTGAATCATGGGCAAGTATTTGGCGTCAAAAAGCAACCAAAGAACAAGT
AAGTCCTCAATTCAGTCAGATGTTTCATGCACCATATGAATTGA >
GAGCTAACATCCCAGTACGTAATTTCCAAGAATTTTATGATGCCTTTGGTG
TTAAAAAAGGCGATTCAATGTATCTAAAACCAGAAAAACGTTTGACACTTT
GGTAA

MGDYYGKKYFGAAKKDVEHMAKKIINVYKTRLKNNTWLSENTKAMAICK
LDNMRLMIGYPDYPDLRQYQFDSKASFFENNDNYRKLSNKKTFEEFNQSNQ
REHWQMSANAVNAYNDPNTNSIVFPAAIFQSPLYDKTKTVSQNYGAIGAIIIGH
EISHSFDINGMKYDEKGNLHDWWTKEDLNHYKKSTQAMIDQWDGLKADGG
KVDGKLTLENIADNGGVMASLEALKTEKIQTIKNFLNHGQVFGVKKQPKNK
VSPQFSQMFMHHMN*

Sequence description:

A] Length: 819 bp - 272 aa (full length gene)
(107 bp of additional DNA sequence (> onwards) is
also included. While not in-frame with the
described orf, it also shares strong homology
with the neutral peptidases.

FIG. 1_{CONT'D}

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B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-89 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-89 gene sequence. ID-89 and ID-170 together show homology over their combined entire length with the neutral endopeptidases from *Lactococcus* and *Lactobacillus*. Possesses TTG (possible ATG start codon located 13 bp further downstream) start codon with no obvious signal peptide. Shine Dalgarno sequence not immediately obvious. Possibly located further downstream

ID-171

Clone 2-18/22b (Mod2)

ATGACCATGATTACGCCAAGCTTCATTAAGGTATCTCTAGATGAAACAAAT
CGTATGATGCGTATGATATCAGATTTATTAAGTTTATCGCGCATTGATAAT
GAAGTAACGCATTTAGATGTTGAAATGACGAATTTTACAGCTTTCATGACC
TCAATTTTGAATCGATTTGATCAGATTAGAAATCAAAAAACAGTCACAGG
AAAAGTTTATGAAATTGTCAGAGATTATCCTCTTAAGTCAATTTGGGTGGA
AATTGATACAGATAAGATGACTCAAGTGATTGATAACATTTTAAATAATGC
AGTCAAGTATTCACCAGATGGTGGTAAGATTACAGTTAATCTACGCACAAC
TAAAACGCAGATGATTTTATCAATATCAGACCAAGGCTTAGGTATTCCCAA
AAAAGATTTACCTCTCATTTTTGATCGTTTTTATCGTGTTGATAAGGCGAGA
AGTCGTCAACAGGGTGGGACTGGACTTGGTTTGTCAATTGCAAAAGAAAT
TGTTAAGCAGCATAAGGGATTTATTTGGGCTAAGAGTGAGTATGGTAAAG
GGTCTACTTTTACAATCGTCTTGCCCTTATGATAAAGATGCTGTAACCTTATGA
AGAATGGGAGGACGTTGAAGATTAA

MTMITPSFIKVSLEDETNRMMRMISDLLSLSRIDNEVTHLDVEMTNFTAFMTSIL
NRFDQIRNQKTVTGKVYEIVRDYPLKSIWVEIDTDKMTQVIDNILNNAVKYSP
DGGKITVNLRTTKTQMILSISDQGLGIPKKDLPLIFDRFYRVDKARSRQGGGTG
LGLSIAKEIVKQHKGFIWAKSEYGKGSTFTIVLPYDKDAVTYEEWEDVED*

Sequence description:

- A] Length: 613 bp - 212 aa (full-length gene possibly)
- B] Possible Shine Dalgarno sequence present upstream of a ATG start codon. May not have yet determined the N- portion of this gene. No obvious signal peptide.

FIG. 1 CONT'D

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ID-172

Clone 2-54balternate (107b)

TTGAAAAAATTATTACTTCTATTCTATTACTTAGTTGCATTTTTTTTATGC
CAACCATCTCTGCTGAATCTTTTAATGCTTCCGCTAAACATGCCTTAGCAGT
TGATTTAGATTTCAGGAAAAATCTTGTATGAAAAAGATGCTAACAAACCCG
CTGCTATTGCTTCCTTGACTAAAATAATGACCGTTTATATGGTCTATAAAG
AAATTGATAACGGTAACCTCAAGTGGAAATACCAAAGTAAATATATCTGAC
TACCCTTATCAACTAACACGCGAATCTGATGCTAGTAATGTTCCCTTTAGAA
AAAAGGCGCTATACTGTTAAACAACCTCGTGGACGCTGCCATGATTTCTAGT
GCTAACAGTGCAGCCATTGCTTTAGCTGAACATATTTTCAGGAAGTAAAGT
AAATTTGTTGATAAAATGACTGCTCAATTGGAAAAGTGGGGAATTCATGAT
AGCCACCTAGTCAATGCTTCTGGCTTAAATAATAGTATGTTAGGCAATCAC
ATTTATCCAAAATCGTCACAAAACGACGAAAATAAAATGAGTGCACGTGA
TATTGCTATTGCTGCCTACCATTTGGTCAACGAATATCCTTCCATTCTTAAG
ATTACTAGTAAGTCCGTTGCTAAATTTGATAAAGATATTATGCATTCTTAT
AACTACATGCTACCAGATATGCCTGTCTTTAGACCAGGTATTACAGGTTTG
AAAAGTGGGACAACGGAATTAGCTGGCCAATCTTTTATTGCTACATCTACT
GAAAGTGGAAATGAGACTACTCACTGTTATTATGCATGCTGATAAGGCCGAT
AAAGACAAATATGCTCGCTTTACAGCAACTAACTCTCTCTTGAACATATC
ACAAACACCTACGAACCTAACCTTGTATTAGCTAAAGGAGCTGCATATAA
AGGTAAAGAAGCAAGTGTGAGAGACGGAAAAGAACAATCGGTCATCGCT
GTTGCTAAAAACGATTTGAAAGTAGTACAGAAGAAAAATATCACTAAACA
AAATCAGTTAAAAATTAACTTTAAAAAAGAGCTTACTGCTCCTATTACAAA
AAAAGAGAACCTAGGGAAAGCTTATTACGTTGACCTTAATAAGGTTGGAA
AAGGCTATCTCATAAAGGAACCTAGCGTTTATTTAGTGGCAAAAGATAGT
ATTGAGCGCAGTTTCTTCTCAAAGTGTGGTGGAAATCATTTTGTGCGCTAC
GTTAACGAAAACTTTAA

MKKIITSILLSCIFFMPTISAESFNASAKHALAVDLDSGKILYEK DANKPAAIA
SLTKIMTVYMVYKEIDNGNLKWNTKVNISDYPYQLTRESNASNVPLEKRRT
VKQLVDAAMISSANSAALAEHISGTESKFVDKMTAQLEKWGIHDSHLVNA
SGLNNSMLGNHIYPKSSQNDENKMSARDIALAA YHLVNEYPSILKITSKSVAKF
DKDIMHSYNYMLPDMPVFRPGITGLKTGTTELQSFATSTESGMRLLTVM
HADKADKDKYARFTATNSLLNYITNTYEPNLVLAKGAA YKGKEASVRDGKE
QSVIAVAKNDLKVVQKKNITKQNQLKINFKKELTAPITKKENLGKAYYVDLN
KVGKGYLIKEPSVHLVAKDSIERSFFLKVWWNHFVRYVNEKL*

FIG. 1 CONT'D

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Sequence description:

- A] Length: 1236 bp - 412 aa (full-length gene sequence possibly)
B] A possible Shine-Dalgarno sequence precedes the putative 'TTG' start codon. (needs further cloning and sequencing to verify N-terminus)

ID-173

Clone 3-60b

ATGACGCTTCGAGAATTAACAATAGAAGAATTTAAAGAACATTCAGGAAA
TTATGATTCACAATCATTTTTACAAACACCTGAGATGGCTAAACTTTTAGA
AAAACGCGGCTATGATGTTAGGTATTTGGGATATCAAGTAGAAAATAAAC
TAGAGATAATCAGTTTATCTTATATTATGCCAGTCACTGGTGGTTTTCAAAT
GAAAATTGATTCAGGACCAGTTCATTCAAATTCTAAGTATCTAAAACAATT
TTATAAAGCATTGCAAGGCTATGCCAAATCCAACGGTGTCTAGAATTAAT
AGTTGAGCCTTTTGATGATTACCAATTATTCAGTTCGGGAGTTCCTAGT
AATCAGGGAAATGATAATCTGATTGAAGATTTTACCAGTTCAGGTTATCAC
CATGATGGTTTAAACAACTGGTTTTACTGGTAAATATTTATCTTGGCACTATG
TTAAAAATTTAGAAGGTGTCACTTCTGAAACGTTACTATCTTCATTCTCTAA
GACAGGACGAGCTTTGGTTAAGAAAGCAATGTCTTTTGAATCAAGGTTT
CGGTTCTTAAACGTGATGAGCTACATTTATTTAAAGAGATAACAACCTTCTA
CGTCAAATAGACGTGATTATATGGATAAGTCCTTAGATTATTATCAAGATT
TTACGATAGCTTTGAAGGCAAGGCTGAATTTGTGATTGCCACTTTAAATT
TTAGAGAATACGACCATAACTTGCAAATAAAAGCTGAAGCATTGGAAAAT
AAGCTT

MTLRELTIIEFKEHSGNYDSQSFLQTPEMAKLLEKRGYDVRYLGYQVENKLEI
ISLSYIMPVTGGFQMKIDSGPVHSNSKYLKQFYKALQGYAKSNGVLELIVEPF
DDYQLFTSSGVPSNQGNLIEDFTSSGYHHDGLTTGFTGKYLSWHYVKNLE
GVTSETLLSSFSKTGRALVKKAMSFQIKVRVLKRDELHLFKEITTSTSNRRDY
MDKSLDYYQDFYDSFEGKAEFVIATLNFREYDHNLQIKAEALENKL

Sequence description

- A) Length: 771 bp - 257 aa (partial gene sequence)
B) This gene sequence was not identified using the LEEP system. It was identified immediately downstream of the ID-65 gene which was identified by

FIG. 1 CONT'D

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LEEP, during cloning and sequence analysis of the full-length ID-65 gene sequence. Sequence Characteristics:
No obvious leader peptide sequence
Orf is preceded by a potential Shine-Dalgarno sequence.

ID-174

Clone 2-17b (ID-80b)

TTGTCATTAAGTTTGGTTGCAGTGTTAAATCTTATCCCTCCTAAAATCATGG
GATCAGTTATTGATGCTATTACAACCTGGAAAATTAACAAGACCACAATTAC
TATGGAATTTATTAGGTTTGGTTTTGTCAGCTTTAGCTATGTATGGGCTGCG
TTATATTTGGCGTATGTATATTTTAGGGACTTCTTACAAATTAGGCCAAGTT
GTCAGATACCGTTTATTTGAACATTTTACAAAAATGTCTCCTTCTTTTTATC
AGAAATATCGTACAGGTGATTTAATGGCGCACGCGACCAACGACATCAAT
TCTCTAACACGTCTTGCAGGAGGAGGAGTTATGTCAGCAGTGGATGCCTCT
ATCACAGCATTAGTAACGCTTATCACCATGTTCTTTACTATTTTCGTGGCAA
ATGACATTAATTGCGGTTATCCCTTTGCCCTTAATGGCCTTAGCACTAGTA
AATTGGGGCGAAAAACCCATGAAACCTTCAAAGAATCTCAGGCAGCCCTT
TTCAGAATTAAATAATAAAGTG

MSLSLVAVLNLIPPKIMGSVIDAITTGKLTRPQLLWNLLGLVLSALAMYGLRYI
WRMYILGTSYKLGQVVRYRLFHFHTKMSPSFYQKYRTGDLMAHATNDINSLT
RLAGGGVMSAVDASITALVTLITMFFTISWQMTLIAVIPLPLMALALVNWGEK
PMKPSKNLRQPFSLENNKV

Sequence description

A) Length: 534 bp - 178 aa (partial gene sequence)

B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-80 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-80 gene sequence.

Sequence Characteristics:

No obvious leader peptide sequence

Orf is preceded by a potential Shine-Dalgarno sequence.

FIG. 1 CONT'D

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ID-175

Clone 2-11Ab (ID-103b)

ATGCATATTGAGACTGTTATTGATTTCAAAGAATTAGGAAAAAGATATCGT
TTAAAAATCCTACAAAAGAATTAATAGCTGATACTTTAGAACAAGTCTTA
GAAGTGATAAAAGAAGTTGATTATTATCAATCTCAAAATTATTATGTTGTT
GGTTATTTATCTTATGAAGCATCTGCTGCTTTTGATTACATTTTAAAGTTT
CTCAACAGAAGTTGGCTGGAGAACATCTAGCTTATTTTACAGTACATAAAG
ATTGTGAGAACGAAGCTTTTCCTTTAAGTTATGAAAATGTTAGATTAGCAG
ATAATTGGACTGCTAATGTTTCTGAGCAAGAATATCAAGAGGCAATTGCTA
ATATTAAAGGACAAATTAGACAAGGAAATACTTATCAAGTAAATTATACA
CTAGAGCTTAGCCAACAATTATGCTCGGATCC

MHIETVIDFKELGKRYRFKNPTKELIADTLEQVLEVIKEVDYYQSQNYVVG
LSYEASAAFD SHFKVSQQLAGEHLAYFTVHKDCENEAFPLSYENVRLADNW
TANVSEQEYQEAIANIKGQIRQGNTYQVNYTLELSQQLCSD

Sequence description:

- A] Length: 440 bp - 146 aa (partial gene sequence)
B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-103 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-103 gene sequence. Shine Dalgarno sequence present upstream of ATG start codon, No apparent leader peptide sequence

ID-176

Clone 2-18/22b(b) (ID-104b)

GTGAATAATATGTTTTATCTCAAAATAGCCTGGCATAATTTAAAACATTCT
ATAGACCAGTACATACCATTCTCTTAGCCAGTTTATTACTTTATTTCATTGA
CTTGTTCTACGCTACTAATCTTAATGAGTGCTGTTGGAAGAGATATGGGGA
CAGCGGCAACGGTTCTTTTCTTGGAGTGATTGTTTTGTCAATCTTTGCGGT
AGTCATGGAACATTATAGCTACAATATCTTGATGAAACAGCGTAGTAGTG

FIG. 1_{CONT'D}

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AATTTGGACTGTATAACATTTTGGGGATGAATAAACGTCAAGTTGCGCGTG
 TAGCTAGTCTAGAGCTGTTTATTATTTATATATTTCTTATTTCTATAGGAAG
 TCTGTTTAGTGCTTTTTTTGCTAAATTTATTTATTTAATTTTTGTCAACATTA
 TTAACATCATGCACTAAATCTTAGTTTAAGTTTATGGCCATTTATTATTTG
 TATCGTTATATTTACAGGTATTTTTCTGACTTTAGAAGTTCCAGTTATTCGA
 CATGTTCAATTTATCATCCCCATTAAGTCTTTTTAGAAAGAAACAACAGGGA
 GAAAAAGAACCAAAAGGTAATCTTATACTTGCAATTTAGCGTTAGTAGCT
 ATCGCCATCGCTTATACAATGGCTCTTACTTCAGGTAAAGCACCTGCATTA
 GCTGTTATCTATCGTTTCTTCTTTGCAGTACTTTTAGTAATTGCTGGTACTT
 ATCTTTTTTATATTAGTTTTATGACATGGTACTTAAAAAGGTTGCGTCAAAA
 CAAGCATTATTATTATAAATCTGAGCATTTTGTATCAACTTCGCAAATGAT
 TTTTCGAATGAAGCAAAATGCAGTAGGGTTAGCAAGTATCACTTTATTAGC
 TGTTATGGCTCTAGTTACTATTGCTACAACAGTCTCACTCTATTCAAATACA
 CAAAATGTTGTTACCGGACTATTTCCAAAATCAGTAAGTTTATCAATAGAT
 AATTCAAAAGGTGACGCGAAAAATATATTTGAAGAAAAGATTTTGAAGAA
 ACTAGGTAAGTCATCTAAGGAAGCTATCACTTATAATCAGACAATGATTTC
 GATGCCAGTTAGTCAATCAAGTGACTTAATATCACATCTA

MNNMFYLKIAWHNLKHSIDQYIPFLASLLLYSLTCSTLLILMSAVGRDMGTA
 ATVFLGVIVLSIFAVVMEHYSYNILMKQRSSEFGLYNILGMNKRQVARVASL
 ELFIYIFLISIGSLFSAFFAKFIYLIFVNINYNHALNLSLSLWPFICIVIFTGIFLTLE
 VPVIRHVHLSSPLSLFRKKQQGEKEPKGNLILAILALVAIAIAYTMALTSGBKAP
 ALAVIYRFFFAVLLVIAGTYLFYISFMTWYLKRLRQNKHYYYKSEHFVSTSQM
 IFRMKQNAVGLASITLLAVMALVTIATTVSLYSNTQNVVTGLFPKSVSLSIDNS
 KGDAKNIFEKILKKLGKSSKEAITYNQTMISMPVSQSSDLISHL

Sequence description:

- A] Length: 1119 bp - 373 aa (partial gene sequence)
- B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-104 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-104 gene sequence. Possible Shine Dalgarno sequence present upstream of a GTG start codon. Possesses a potential leader peptide sequence

ID-177

FIG. 1^{CONT'D}

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Clone 2-5b (ID-112b)

ATGGTTGAGCCAATTATTTCAATACAAGGACTTCATAAAAGTTTTGGGAAA
AATGAGGTTTTAAAAGGCATTGACTTGGATATTCATCAAGGAGAAGTGGT
GGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTTAAGAACAAT
GAATCTCTTGGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGATTG
ATATAACAGACAAAAAGAATGATATTTTTAAAATGCGCGAAAAAATGGGC
ATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAT
ATTACTTTATCACCTATTAAGACAAAGGGACTTTCTAAGCTTGATGCTCAG
ACAAAAGCATACGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAA
TGCTTATCCAGCAAGCTTATCTGGAGGACAACAACAACGGATTGCTATTGC
AAGAGGTCTTGCAATGAATCCTGATGTCCTTCTTTTGGATGAACCTACTTCA
GCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTA
GCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCA
CGTGAAGTAGCGGATCGTGTCAATTATGGATGCAGGGATTATTGTTGAG
CAAGGGACCCCTAAGAAAGTATTTGAGCAGACAAAAGAAATCCGCACAAG
AGACTTCTTAAGTAAAGTATTATAA

MVEPIISIQGLHKSFGKNEVLKGIDLDIHQGEVVVIIGPSGSGKSTFLRTMNLE
VPTKGTVTFEGIDITDKKNDIFKMREKMGVMVFQQFNLPNMTVLENITLSPIKT
KGLSKLDAQTKAYELLEK VGLKEKANAYPASLSGGQQQRIAIARGLAMNPDV
LLFDEPTSA LDPEMVGEVLTVMQDLAKSGMTMVIVTHEMGFAREVADRVIF
MDAGIIVEQGT PKKVFEQTKEIRTRDFLSKVL*

Sequence description:

- A] Length: 735 bp - 244 aa (full length gene)
B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-112 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence precedes the 'ATG' start codon. No obvious leader peptide

ID-178

Clone 2-5c (ID-112c)

FIG. 1^{CONT'D}

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ATGTCTCA_sTATCAAGAGTGGTTAGAAAACGACTCACTCGGTAAAGATATT
AAGTCAGATTTAGAAGCTATTAAAGGAGATGAATCTGAAATTCAGGATCG
TTTTTACAAAACATTAGAATTTGGAACGGCGGGATTGAGAGGTAAACTTG
GAGCAGGAACCAATCGTATGAATACTTATATGGTGGGGAAAGCAGCACAA
GCATTAGCTAATCGATTATTGATCATGGCCCTGAAGCTATTGCACGTGGAA
TTGCAGTTAGTTATGATGTCCCGTTATCAATCTAAGGAATTTGCAGAATTA
ACTTGGTCCATTATGGCAGCAAATGGTATTAAAGCCTTATATTTA

MSHMNYKEYQEWLEND_sLGKDIKSDLEAIKGDSEIQDRFYKTLEFGTAGLR
GKLGAGTNRMNTY_sMVGKAAQALANRL_sLIMALKLLHVELQLVMMSRYQSKE
FAELTWSIMAANGIKALYL

Sequence description:

- A] Length: 366 bp - 122 aa (partial gene sequence)
B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-112 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence preceded the 'ATG' start codon. No obvious potential leader peptide sequence.

ID-179

Clone 2-5d (ID-112d)

ATGCAACCTGTAAAAGTCGATGAACCTTCTGTTGAAGAAACCATTACTATT
TTGAAAGGTATCCAAAAAAATACGAAGATTATCATCACGTAAAAATATAA
TAATGATGCCATAGAAGCAGCTGCAGTACTATCTAATCGTTATATCCAAGA
CCGCTTTTACCTGATAAAGCAATAGACTTATTAGATGAAGCTGGTTCTAA
AATGAACCTAACACTAAATTTTGTGATCCAAAAGAAATTGATCAACGTCT
CATTGAAGCAGAAAATTTAAAAGCGCAAGCGACTCGTGAAGAAGATTACG
AACGTGCAGCTTACTTCCGTGACCAGATTGCAAAATATAAAGAAATGCAG
CAACAAAAGGTGACGATCAAGATACACCTATTATTACCGAAAAACAAT
TGAGCACATCATTGAAGAAAAAACGAATATCCCTGTTGGTGATTTAAAAG
AAAAAGAACAATCTCAATTAATTAATCTCGCAGATGACTTGAAACAGCAT
GTGATCGGCCAGGATGACGCTGTCATTAAGATTGCAAAAGCTATTTCGTCT
AATCGAGTTGGTCTTGGTAGCCCAAACCGTCCTATTGGTTCCTTTTATTTG
TAGGACCAACCGGTGTTGGTAAACTGAACTTTCTAAACAAC_sTAGCAATTG
AGCTCTTTGGTTCAGCTGATAGTATGATTCGTTTTGATATGTCAGAGTACAT
GGAAAAGCATGCTGTTGCTAAATTAGTCGGAGCGCCTCCAGGATACGTGG
GATACGAGGAAGCTGGACAAC_sTAAGTGAAGGTTTCGTGAAATCCTTAC
TCGCTCATCCTTCTAGATGAAATTGAAAAAGCTCATCCCGATGTCATGCAT

FIG. 1_{CONT'D}

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ATGTTCTTGCAGGTCCTTGATGACGGTCGATTAAACAGATGGACAAGGAAG
 AACTGTTAGTTTTAAAGATACCATTATCATCATGACCTCAAATGCTGGTTC
 TGGTAAAACCTGAAGCAAGTGTTGGCTTTGGTGCCTCACGAGAAGGTAGGA
 CGAATTTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCAT
 GCAAGC

MQPVKVDEPSVEETITILKGIQKKYEDYHHVKYNND AIEAAAVLSNRYIQDRF
 LPDKAIDLLDEAGSKMNLTLNFVDPKEIDQRLIEAENLKAQATREEDYERAAY
 FRDQIAKYKEMQQQKVDDQDTPITEKTIEHIEEKTNPVGD LKEKEQSQ LNL
 ADDLKQHVIGQDDAVIKIAKAIRNRVGLGSPNRPIGSFLFVGPTGVGKTELSK
 QLAIELFGSADSMIRFDMSEYMEKHAVAKLVGAPPGYVGYEEAGQLTEKVR
 NPYSILLDEIEKAHPDVMHMF LQVLDDGRLTDGQGRTVSFKDTIIMTSNAGS
 GKTEASVGF GASREGRTNSSSVPGDPLESTCRHAS

Sequence description:

A) Length: 1070 bp ÷ 356 aa (Partial gene sequence)

B) This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-112 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence preceded the 'ATG' start codon. No obvious potential leader peptide sequence.

ID-180

Clone 2-7b (ID-113b)

ATGAGAGGGAAGGTTATTTACGGCACAACCCTTATAGGTCTTTTTCTATTC
 TTATTTTTCTATTTTTGGATTCTTAAGCATCACATCGAGAGAATACATCATC
 ATCGTATAAAGCAGGTAGATGCGAAGAGTGATTAAACAGGATTTAAACC
 CATTTGCCATTATCAGCATTGATACAAAGCAACAAGTTATTCCTCTTGTT
 ACAAAGAAGGCGGAAAATATGTCAAAGCTAGGGATAATATTAATGTTGA
 TATCGAATTACGGGATTCTCCAAGTAGATCACATCATTTATCAGAAAAGCC
 GAGAATTAGGACAAAAGGTTAATATCATATAGAGGAAATTCCTCTCGTT
 ACTTTGATAAGAAGTCATTGAAAAGTTAAGTTTGTTACTAATAAGTTAAAGG
 AAAAGAAGCATCGATTAGCAGGAATGCCTAAAGAATCGGAGTGGGTATTG
 CATGGTCCCTTTCTAGACAGAACATTATTAAGAAATTATCTGAGTTATAAT

FIG. 1 CONT'D

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ATTGCTGGTGAGATTATGCCTATGCCCCAAACGTTGCTACTGTGAGTTAT
TTGTCAATGGTGAGTATCAGGGAG

MRGKVIYGTTLIGLFLFLFFYFWIPKHHIERIHHRKQVDAKSDLTGFKTHLP
SIDTKQQVIPLVTKEGGKYVKARDNNVDIELRDSPSRSHLSEKPRIRTKGLIS
YRGNSSRYFDKSLKVKFVTNKLKEKKHRLAGMPKESEWVLHGPFLDRTLLR
NYLSYNIAGEIMPMPQTFATVSYLSMVSIRES

Sequence description:

- A) Length: 582 bp - 194 aa (Partial gene sequence)
B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-113 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-113 gene sequence. ATG start codon is preceded by a Shine-Dalgarno sequence-Possesses a potential leader peptide sequence. C-terminus to be determined.

ID-181

Clone 2-17b (ID-117b)

CTTCACATTTTATTGATCACTATCTGACAAATGTTAATCAAACAGCAGTTCT
TATTTTAGTGGGATATTATTCAATGTATGTCTTGCAGACCTTAATTCAATAT
TTTGGGAATCTCTTTTTTGC GCGTGTCTTATAGTATTGTTAGAGATATTC
GTAGAGATGCTTTTGCTAATATGGAAAGGCTAGGCATGTCTTATTTTGATA
GGACACCGGCAGGATCTATTGTGTACGTATTACTAATGATACTGAAGCAA
TATCTGATATGTTTTCGGGTATTTTATCAAGTTTTATCTCGGCGATATTTAT
TTTTACAGTTACTCTGTACACTATGTTGATGCTAGACATTAACTAACAGG
ACTCGTCGCTCTTTTGTTACCTGTTATCTTTATATTAGTGAATGTCTATCGG
AAAAAATCAGTCACTGTCATTGCTAAAACGAGAAGTTTACTTAGTGATATC
AACAGTAAATTATCAGAAAGTATTGAAGGAATTC

SHFIDHYLTNVNQTA VLILVGYYS MYVLQTLIQYFGNLF FARVSY SIVRDIRRD
AFANMERLGMSYFDRTPAGSIVSRITNDTEAISDMFSGILSSFISAIFIFTVTLYT
MLMLDIKLTGLVALLLPVIFILNVNRYRKS SVTVIAKTRSLSDINSKLSIESIEGI

FIG. 1 CONT'D

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Sequence description:

- A) Length: 498 bp - 165 aa (Partial gene sequence)
 B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-117 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-117 gene sequence. N- and C-termini have yet to be determined

ID-182

Clone 3-8b (ID-120b)

ATGTACCATATTGAATTAAAAAAGGAAGCTTTACTACCAAGAGAACGCCT
 AGTTGATTTAGGCGCAGATAGATTGAGTAATCAGGAGTTATTAGCCATTCT
 CTTACGTACAGGTATTAAAGAAAAACCTGTTCTTGAAATTTCAACGCAAAT
 TTTAGAAAACATAAGCAGTTTAGCAGATTTTGGTCAATTATCCTTACAGGA
 GTTGCAATCCATTAAAGGAATCGGTCAGGTAAATCCGTCGAAATAAAAG
 CTATGCTAGAACTAGCAAAACGGATTCACAAAGCTGAATATGATCGTAAA
 GAGCAAATTTTAAGTAGTGAACAATTAGCGAGGAAAATGATGCTCGAATT
 AGGGGATAAAAAACAAGAACATTTAGTAGCTATTTATATGGATACACAAA
 ATCGTATTATCGAACAGAGAACTATTTTTATTGGTACTGTACGTCGTTTACG
 TAGCAGAGCCAAGAGAAATTCTACATTATGCTTGTA AAAACATGGCAACT
 TCTTTGATTATTATACATAATCATCCCTCAGGTTCTCCAAATCCCAGTGAAA
 GTGATTTAAGTTTCACTAAAAAAAATAAAACGATCATGTGATCATCTGGGAA
 TTGTCTGCCTAGATCACATCATCGTTGGAAAAAATAAATATTATAGTTTTC
 GAGAAGAAGCAGATATTTTATAA

MYHIELKKEALLPRERLVDLGADRLSNQELLAILLRTGIKEKPVLEISTQILENI
 SSLADFGQLSLQELQSIKGIGQVKSVEIKAMLELAKRIHKA EYDRKEQILSSEQ
 LARKMMLELGDKKQEHLVAIYMDTQNRIIEQRTIFIGTVRRSVAEPREILHYAC
 KNMATSLIIHNHPSGSPNPSESDLSFTKKIKRSCDHLGIVCLDHIVGKNKYYSF
 REEADIL*

Sequence description:

- A) Length: 681 bp - 227 aa (full-length gene)
 B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-120 gene which was identified by LEEP,

FIG. 1 CONT'D

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during cloning and sequence analysis of the full-length ID-120 gene sequence.
ATG start codon is preceded by an typical
Shine-Dalgarno sequence. No obvious leader
peptide sequence

ID-183

Clone 3-11b (ID-121b)

TGGTTAAAAGTAGTGATAGCTTGTATTCCATCTATTTTAATTGCTTTACCAT
TTGATAATTGGTTTGAAGCTCATTTTAATTTTCATGATTCCGATTGCAATAGC
CCTAATCTTTTATGGTTTTGTCTTCATATGGGTTGAAAAACGTAATGCACAC
CTCAAACCACAGGTAACCGAATTGGCAAGTATGTCTTACAAGACAGCTTTC
TTGATTGGATGTTTCCAGGTTCTCAGTATTGTTCCGGGAACCAAGTCGTTCTG
GAGCTACTATTTTAGGAGCAATTATTATTGGAACTAGTCGTTCCGGTCGCTG
CTGACTTTACTTTCTTCCTTGCCATCCCAACTATGTTTGGTTATAGTGGACT
TAAGGCGGTTAAATATTTTTTAGATGGTAACGTCTTGAGTTTAGACCAATC
TTTAATACTTTTAGTAGCAAGTCTGACAGCTTTCGTAGTTAGTTTATATGTT
ATTCGTTTCTTGACAGACTATGTCAAACGACACGATTCACCATCTTTGGT
AAGTATCGTATAGTCTTAGGAAGTTTACTCATCCTCTACTGGTTAGTTGTTT
ATTTATTCTAA

WLKVVIACIPSILIALPFDNWFEAHFNFMPIAIALIFYGFVFIWVEKRNAHLKP
QVTELASMSYKTAFLIGCFQVLSIVPGTSRSGATILGAIIGTSRSVAADFTFFLA
IPTMFGYSGLKAVKYFLDGNVLSLDQSLILLVASLTAFFVVSLEYVIRFLTDYVKR
HDFTIFGKYRIVLGSLLILYWLVVHLF*

Sequence description:

- A) Length: 579 bp - 193 aa (partial sequence)
- B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-68 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-68 gene sequence described in WO 00/06736. N-terminus has yet to be determined.

ID-184

Clone 3-11c (ID-121c)

FIG. 1 CONT'D

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ATGGAAATGAAACAAATCAGTGAAACAACACTGAAAATTACAATTAGTAT
GGAAGATTTAGAAGATCGTGGTATGGAGCTGAAAGATTTCTAATCCCTCA
GGAGAAGACTGAGGAATTTTCTATTCTGTCATGGATGAATTAGACTTGCC
AGAAAACTTTAAAAATAGTGGTATGTTAAGTTTTCGAGTAACACCTAAAA
AAGATCGCATTGATGTTTTGTTACAAAGTCTGAATTAAGTAAAGATTTAA
ATTTAGAAGAATTAGCAGATTTGGGTGACATTTCAAAAATGTCTCCAGAAG
ACTTTTTTAAAACCTTGGAACAATCGATGTTGGAAAAAGGGGATACGGAT
GCCCATGCCAAATTAGCAGAAATTGAAAATATGATGGATAAAGCAACTCA
AGAAGTAGTTGAGGAAAATGTTTCTGAAGAACAACCTGAAAAGGAAGTAG
AAACGATTGGATATGTTCACTATGTCTTTGATTTTGATAATATGAAGCTGT
AGTTCGATTTTCACAAACGATTGATTTTCCAATAGAAGCTT

MEMKQISEITLKITISMEDLEDRGMELKDFLIPQEKTEEFFYSVMDELDLPENF
KNSGMLSFRVTPKKDRIDVFVTKSELSKDLNLEELADLGDISKMSPEDFFKTL
QSMLEKGDTHAKLA EIENMMDKATQEVVEENVSEEQPEKEVETIGYVHY
VFDFDNIEAVVRFSQTIDFPIEA

Sequence description:

- A] Length: 547 bp - 182 aa (Partial sequence)
B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-68 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-68 gene sequence. ATG start codon is preceded by an typical Shine-Dalgarno sequence. No obvious potential leader peptide sequence

ID-185

Clone 3-16b (ID-122b)

GGAAACCAACGGCCAGTACAATCGTCAAGGGTAGATTATCCTAAACGTAG
TCGTGCCAAGATTGTAGAAGTTTATTTTAGACAAGCTTCTACTACTGATTA
TTCTGGTGTTTACAAAGGTTACTATATTGACTTTGAAGCCAAAGAAACCCG
GCAGAAAACCTGCTATGCCTATGAAAAATTTTCATGCTCACCAAATAGAGC
ACATGGCAAATGTATTACAGCAAAAAGGGATTGCTTTGTCTTGCTTCATT

FIG. 1_{CONT'D}

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TTTCCACACTTAAGGAAACCTATCTACTCCCTGCTAATGAGTTAATTTTCATT
TTATCAGATTGATAAAGGCAATAAATCAATGCCTATTGATTATATCAGAAA
AAATGGATTTTTTCGTAAAGGAGAGTGCCTTTTCCTCAAGTCCCTTACTTAGA
TATTATTGAAGAAAAATTATTAGGCGGTGATTACAATTAA

GNQRPVQSSRVDYPKRSRAKIVEVYFRQASTTDYSGVYKGYIDFEAKETRQ
KTAMPMKNFHAHQIEHMANVLQQKGICFVLLHFSTLKETYLLPANELISFYQI
DKGNKSMPIDYIRKNGFFVKESAFPQVPYLDIIEKLLGGDYN*

Sequence description:

- A] Length: 447 bp - 149 aa (partial sequence)
B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-122 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-122 gene sequence. N-terminus has yet to be determined

ID-186

Clone 3-17b (ID-123b)

GGATCCTAAAAACGCTAAGGTTTATCAAAAAAATGCTGATCAATTTAGTG
ACAAGGCAATGGCTATTGCAGAGAAGTATAAGCCAAAATTTAAAGCTGCA
AAGTCTAAATACTTTGTGACTTCACATACAGCATTCTCATACTTAGCTAAG
CGATACGGATTGACTCAGTTAGGTATTGCAGGTGTCTCAACCGAGCAAGA
ACCTAGTGCTAAAAAATTAGCCGAAATTCAGGAGTTTGTGAAAACATATA
AGGTAAAGACTATTTTGTGGAAGAAGGAGTCTCACCTAAATTAGCTCAAG
CAGTAGCTTCAGCTACTCGAGTTAAATTGCAAGTTTAAGTCCTTTAGAAG
CAGTTCCCAAAAACAATAAAGATTACTTAGAAAAATTTGGAACTAATCTTA
AGGTACTTGTCAAATCGTTAAATCAATAG

DPKNAKVYQKNADQFSDKAMAIAEKYKPKFKAASKYFVTSHTAFSYLAKR
YGLTQLGIAGVSTEQEPSAKKLAEIQEFVKTYKVKTIFVEEGVSPKLAQAVAS
ATRVKIASLSPLEAVPKNNKDYLENLETNLKVLVKS LNQ*

Sequence description:

FIG. 1 CONT'D

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A) Length: 433 bp - 144 aa (partial sequence)

B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-123 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-123 gene sequence. N-terminus has yet to be determined

ID-187

Clone 3-46/47 (ID-130b)

ATGAAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAACGCCTCAGA
 AACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATTGG
 ATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTATGCT
 TGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAAA
 TGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATCTGATG
 CCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTGGAAAAA
 TGAAAGGTATTCAAAAAAAGTGAATTAACAGCAGATAACTCATATTTCT
 AAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCA
 GAAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAACCCC
 ACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGG
 AGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGGACGTTCTAT
 CTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGC
 ACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAA
 AAAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGG
 AGAATAA

MKKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGME
 KADKGTALVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQ
 KTELKQQITHISKVVDLENQLDKFVSGYSEGMKRRLSLAIALLGNPVLILDEP
 TVGIDPSLRRIWQELINIKDEGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTP
 LHLKKQFNVSTIEEVFLKAEGE*

Sequence description:

A) Length: 717 bp - 239 aa (Possible full-length sequence)

B) This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-130 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-130 gene sequence. ATG start codon is preceded by a possible

FIG. 1 CONT'D

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Shine-Dalgarno. No obvious potential leader
peptide sequence

ID-188

Clone 3-83b (ID-144b)

ATGGTACAAATGATACATGATATGATTAACAATTGAGCATTGCTGAG
ACACAAGCTGATTTCCAGTGTATGATATTTAGGGGAAGTCCATACTTAT
GGACAACCTAAAGTAGACTCTGACTCTCTAGCTGCTCATATTGATAGCCTA
GGCCTTGTTGAAAAATCACCTGTCTTAGTATTCGGTGGTCAAGAATATGAA
ATGTTGGCGACATTTGTTGCTTTAACAAAGTCAGGGCATGCTTATATACCG
GTTGACCAACACTCTGCTTTGGATAGAATACAGGCTATTATGACAGTTGCT
CAACCAAGCCTTATCATTTCAATTGGTGAATTCCTCTTGAAGTTGATAAT
GTCCAATCCTAGACGTTTCTCAAGTTTCAGCTATTTTGAAGAAAAGACT
CCTTATGAGGTAACACATTCTGTAAAGGTGATGATAATTACTATATTATT
TTCACCTCAGGGACTACTGGTTTACCAAAAGGTGTGCAAATTCACATGAC
AATTTATTGAGCTTTACAAATTGGATGATTTCTGATGATGAGTTTTCAGTTC
CTGAAAGACCGCAAATGTTGGCTCAACCC

MVQMIHDMIKTIEHFAETQADFPVYDILGEVHTYGQLKVDSDSLAAHIDSLGL
VEKSPVLVFGGQYEYMLATFVALTKSGHAYIPVDQHSALDRIQAIMTVAQPSL
IISIGEPLEVDNVPILDVSQVSAIFEEKTPYEVTHSVKGDDNYIIFTSGTTGLP
KGVQISHDNLLSFTNWMISDDEFSVPERPQMLAQP

Sequence description:

- A] Length: 592 bp - 197 aa (partial sequence)
B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-144 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-144 gene sequence. Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. No obvious leader peptide sequence
This orf is not in frame with nuc

ID-189

FIG. 1^{CONT'D}

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Clone 3-86b (ID-145b)

ATGGA AAAATCATCGTTATGAAGATGAAGGTAAATTCAGCGTAAGATGAC
CAGTCGTCATCTCTTTATGTTATCGCTAGGTGGTGTATCGGGACTGGGCTT
TTCTTGAGTTCAGGTTATACCATTGCACAGGCTGGTCCGCTTGGAGCTGTG
CTGTCTTATTTGATTGGTGCCGTTGTGGTTTATTTGGTCATGCTATCACTTG
GGGAATTGGCGGTTGCCATGCCGGTGACGGGGTCATTCCACACTTATGCCA
CTAAGTTTATCAGTCCTGGAACAGGTTTTACTGTTGCTTGGCTATATTGGAT
TTGTTGGACGGTCGCCCTTGGGGACTGAATTTTTAGGTGCTGCCATGCTGAT
GCAGCGCTGGTTCCCAAATGTGCCGGCTTGGGCATTTGCTTCCTTTTTTGCC
CTTGTGATTTTTGGTTTAAATGCTCTTAGCGTACGCTTTTTTG CAGAAGCAG
AGTCTTTCTTCTCAAGTATTAAGGTTATTGCTATCATTATCTTTATTATCTTG
GGCTTAGGTGCTATGTTTGGTCTAGTTTCCTTTGAAGGTCAGCACAAAGGCT
ATTCTCTTCACTCATCTGACTGCCAATGGTGCCTTTCCAAATGGTATCGTTG
CAGTTGTCTCAGTCATGTTGGCTGTTAACTATGCCTTCTCTGGTACTGAGTT
AATTGGTATTGCGGCTGGTGAAACGGATAATCCCAAAGAAGCTGTACCAA
GGGCTATTAAAACGACAATCGGTCGCTTGGTTGTTTTCTTTGTACTGACAA
TTGTTGTCCTAGCTTCGCTATTGCCAATGAAAGAGGCAGGCGTATCCACAG
CACCATTGCTTGATGTCTTTGACAAGATGGGAATCCCTTTTACGGCGGATA
TCATGAAC TTCGTTATCTTGACAGCCATCCTGTCTGCTGGTAACTCAGGTCT
CTACGCATCAAGCCGTATGCTCTGGTCCCTTGCCAATGAAGGTATGTTGTC
AAAATCTGTTGTGAAAATCAATAAACACGGGTGCCCAATGCGTGCTCTTCT
CTTGTC AATGGCAGGAGCAGTGCTGTGCTCTTTTCAAGTATTTACGCTGC
AGACACAGTTTATCTAGCCTTGGTTTCAATCGCGGGCTTTGCTGTTGTTGTC
GTATGGCTAGCCATTCCAGTCGCACAAATCAATTTCCGCAAGGAATTC

MENHRYEDEGKFQRKMTSRHLFMLS LGGVIGTG LFLSSGYTIAQAGPLGAVL
SYLIGAVVVYLVMLSLGELAVAMPVTGSFHTYATKFISPGTGFTVAWLYWIC
WTVALGTEFLGAAML MQRWFPNVPWAFAFFALVIFGLNALS VRFFAEAES
FFSSIKVIAIIIFIILGLGAMFGLVSFEGQHKAILFTHLTANGAFPNGIVAVVSVM
LAVNYAFSGTELIGIAAGETDNPKEAVPRAIKTTIGRLVVFVLTIVVLASLLPM
KEAGVSTAPFVDVFDKMGIPFTADIMNFVILTALSAGNSGLYASSRMLWSLA
NEGMLS KSVVKINKHGVP MRALLSMAGAVLSLFSSIYAADTVYLALVSIAGF
AVVVVWLAIPVAQINFRKEF

Sequence description:

A] Length: 1126 bp - 393 aa (partial gene)

FIG. 1_{CONT'D}

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sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-145 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-145 gene sequence. Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a possible leader peptide sequence.

ID-190

Clone 3-94b

TCAGAAAATGCAGAGGCAGCAACGGTTGCCACAACTTGGTTACCAAAGG
AGCTAATGTCAATTATCGGACCAGCAACATCGGGTGCAGCTGCATCTTCAAC
TCCAAAAGTAAATGCAGCAGCAGTTCCAATGATTGCACCTGCTGCGACAC
AAGACAATTTAGTCTATGGTTCTGATGGAAAAACCTTAAATCAGTATTTCT
TCCGAGCTACTTTTGTGCGATAATTATCAAGGAAAGCTATTGTCTCAGTATG
CTACAGACAACCTTAAAGCTAAAAAAGTTGTTCTATTTTATGATAATTCAT
CAGATTACTCAAAGGGGGTAGCAAAATCATTTAAGGAAAGTTATAGTGGA
AAAATTGTTGATAGTATGACATTCTCCGCTGGTGATACTGATTTCCAAGCG
TCATTGACTAAGTTGAAAGGGAAAGAATATGATGCTATTGTGATGCCAGG
TTACTATACCGAGACAGGATTAATAGTTAAGCAAGCGCGTGATTTAGGTAT
CTCTAAACCGGTTCTTGGGCCTGATGGTTTTGATAGTCCGAAATTTGTGCA
ATCGGCAACACCTGTAGGAGCTTCAAACGTTTATTATTTGACAGGTTTCAC
TACACAAGGATCAACCAAAGCTAAAGCT

SENAEAATVATNLVTKGANVII GPATSGAAASSTPKVNAAAVPMIAPAATQD
NLVYGSDGKTLNQYFFRATFVDNYQGKLLSQYATDNLKAKKVLFYDNSSD
YSKGVAKSFKESYSGKIVDSMTFSAGDTDFQASLTKLKGKEYDAIVMPGYTT
ETGLIVKQARDLGISKPVLGPDGFDSPKFVQSATPVGASNVYYLTGFTTQGST
KAKA

Sequence description

A] Length: 637 bp - 231 aa (partial sequence)

FIG. 1 CONT'D

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B) This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-149 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-149 gene sequence. N- and C-termini have yet to be determined

ID-191

Clone 2-c94b (ID-153b)

TTGGGACTTAAAGACCATGCTTTAGTCTATCCATTTTCATTATCTGGGGGG
CAAAAGCAACGTGTCGCACTAGCTCGTGCGATGATGATTGATCCACAGATT
ATTGGTTATGATGAGCCAACTAGCGCTCTTGATCCAGAGTTGCGTCAAGAA
GTAGAAAACTAATTTTACAAAATAGAGAAACAGGTATGACACAAATTGT
AGTAACACATGATCTTCAATTTGCTGAAAGTATATCTGATACGATTCTCAA
AATTAATCCTAAGTAG

MGLKDHALVYPFSLSGGQKQRVALARAMMIDPQIIGYDEPTSALDPELRQEV
EKLILQNRETGMTQIVVTHDLQFAESISDTILKINPK*

Sequence description

A) Length: 270 bp - 90 aa (partial sequence)

B) This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-153 gene which was identified by LEEP, during cloning and sequence analysis of the ID-153 gene sequence.

N-terminus has yet to be determined

ID-192

Clone 2-c1b (ID-155b)

ATGACTAATATCTCAGATGTTCCAAAAGCTATTAGAACACAGGCACAGTAT
GTTCTCTTGGAATGAGAGTTATGGATCAGTCGGTATTACCGAAAACATAT
AATTCAAAGAACCTTATTTGAAACCAGATATGATTTATATTCATGATAGA

FIG. 1_{CONT'D}

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AGACAAGAGACAATGCTTAAAATCACTCAAGAAATAGAAATGGAGCATTG
A

MTNISDVPKAIRTQAQYVLLGMRVMDQSVLPKTYNSKEPYLKPDMIYIHDRR
QETMLKITQEIMEH*

Sequence description

A) Length: 204 bp - 68 aa (partial sequence)

B) This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-155 gene which was identified by LEEP, during cloning and sequence analysis of the ID-155 gene sequence.

ATG start codon is preceded by a potential typical Shine-Dalgarno sequence.

Has a

typical leader peptide. N-terminus has yet to be verified

ID-193

Clone 2-54altb (ID-172b)

AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCTTGGGGAATATAAATT
TGGATTTTCATGACGATGTAAAGCCAATTTATTCTACGGGAAAAGGTCTAAA
TGAGGCTGTTATTCGTGAGTTATCTGCAGCTAAGGGTGAACCTGAGTGGAT
GTTGGACTTTCGTCTAAAATCCTTGGAACGTTTAATAAAATGCCGATGCA
GACCTGGGGAGCAGATTTATCAGATATTGATTTTGATGATATTATTTATTA
TCAAAAAGCATCTGATAAACCTGCGCGTGATTGGGATGATGTTCCAGAAA
AAATCAAAGAACTTTTGAAAGAATTGGGATTCCAGAAGCTGAAAGAGCC
TATCTTGCAAGGAGCATCAGCACAATATGAATCAGAAGTAGTTTATCACAAT
ATGAAAGAAGAATATGATAAGCTGGGTATTGTTTTTACGGATACTGACTCT
GCACTTAAAGAGTACCCAGAGCTATTCAAAAAATATTTTGCTAAACTTGTC
CCTCCAACAGATAATAAATTAGCTGCTCTGAACTCTGCTGTATGGTCAGGT
GGAACATTTATTTATGTTCCCTAAAGGTGTTAAGGTGGATATTCCACTTCAA
ACTTACTTCCGTATTAATAATGAAAATACTGGACAATTTGAACGTACTCTC
ATTATTGTTGATGAGGGAGCAAGTGTTCACTATGTTGAAGGTTGTACCGCC
CCAACCTTATTCTTCAAATAGTTTACATGCAGCTATAGTTGAAATTTTGCAC
TTGATGGAGCTTATATGCGCTATACGACTATTCAAATTTGGTCCGATAATG
TCTATAATTTAGTGACAAAACGTGCTACCGCTAAAAAAGATGCAACAGTT
GAGTGGATAGATGGAAATCTAGGAGCTAAACAACAATGAAATACCCATC

FIG. 1 CONT'D

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GGTTTACCTTGATGGTGAAGGAGCACGTGGCACGATGTTGTCTATTGCTTT
 TGCAAACAAAGGACAACACCAAGATACGGGTGCAAAGATGATTTCATAATG
 CCCCCATACTAGTTCATCCATTGTCTCTAAATCAATTGCTAAGGGTGGGG
 GAAAAGTTGATTATCGAGGTCAAGTGACATTTAATAAAGATTCCAAAAA
 TCAGTGTACATATAGAATGTGACACCATATTGATGGATGATATTTCAAAA
 TCAGATACCATAACCGTTTAATGAGATTCATAATTACAGGTTGCTTTAGAG
 CATGAAGCAAAGGTGTCTAAGATTTCTGAAGAGCAACTGTACTACTTGATG
 AGTCGAGGTTTATCTGAAGCTGAAGCAACAGAAATGATTGTTATGGGGTTT
 GTTGAGCCCTTTACGAAAGAATTACCAATGGAATATGCGGTAGAGTTAA
 TCGTTTAATTTCTATGAAATGGAAGGTTCAAGTTGGTTAA

MHACRSTLEDLGEYKFGFHDDVKPIYSTGKGLNEAVIRELSAAKGEPEWMLD
 FRLKSLETFNKMPMQTWGADLSDIDFDIIYYQKASDKPARDWDDVPEKIKE
 TFERIGIPEAERAYLAGASAQYSEVVYHNMKEEYDKLGIVFTDTSALKEYP
 ELFKKYFAKLVPPTDNKLAALNSAVWSGGTFIYVPKGVKVDIPLQTYFRINNE
 NTGQFERTLIIVDEGASVHYVEGCTAPTYSSNSLHAAIVEIFALDGAYMRYTTI
 QNWSDNVYNLVTKRATAKKDATVEWIDGNLGAKTMMKYPSVYLDGEGARG
 TMLSIAFANKGQHQDTGAKMIHNAPHTSSSIVSKSIKGGGKVDYRGQVTFN
 KDSKKSVSHEICDTILMDDISKSDTIPFNEIHNSQVALEHEAKVSKISEEQLYYL
 MSRGLSEAEATEMIVMGFVEPFTKELPMEYAVELNRLISYEMEGSVG*

Sequence description:

- A] Length: 1411 bp - 469 aa (Possible full-length gene)
- B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-72 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-72 gene sequence. No obvious Shine Dalgarno sequence upstream of TTG start codon (insufficient sequence data). N terminus needs verification.

ID-194

Clone 3-1b (ID-81b)

ATGATAGAATTCTTTTCTAATATCAGAACAGAGATTCCGCAGATGCCTTTA
 CTTATCCATAGTTTGATTTTATCTGTCTTACCTTTTCTGATGTGGCTGACTTT
 GGTAAATAGAGATAAGCCTTTGTATAAACTATTTGGAGTATCCTTTTAGG
 ACTTCAGTTAATTACGATTTATACTTGGTTTTTCTGGGCAAATTGCCTTTA

FIG. 1 CONT'D

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TCTGAAAGTCTTCCCCTTTACCATTGTCTGAATAGGCATGTTTGTCGGTCTCT
TA

MIEFFSNIRTEIPQMPLLIHSLILSVLPFLMWLTLVNRDKPLYKTIWSILLGLQLI
TIYTWFFWAKLPLSESLPLYHCRIGMFVGLL

Sequence description

A) Length: 261 bp - 87 aa (partial gene sequence)

B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-81 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-81 gene sequence. Sequence Characteristics: Possesses a potential leader peptide sequence. Orf is preceded by a potential Shine-Dalgarno sequence.

ID-195

Clone RS-55b

AAGCTTGTGCAAAGTATTAAAGAGATAGGATTAGCTAATGCGCATTATTA
GCTGTTGCTCCGACAGGGTCAATCAGTTATCTTTCTTCTTGTAAGCCGAGCC
TTCAACCGGTTGTATCACCTGTCTGAAGTACGCAAGGAAGGAGCACTGGGG
AGGGTTTATGTAGCTGCTTATAAGATTGATGCAGATAATTATGTCTACTAC
AAAAAAGGAGCTTATGAAGTGGGATCTGAGGCGATTATCAATATTGCAGC
TGCCGCTCAAAAACACATTGATCAAGCTATTTCTGTTAACGCTTTTCATGAC
AGATCAAGCAACTACGCGAGATTTAAATAAAGCCTATATTCAAGCATTTA
AACAAAAATGTGCCTCTATTTATTATGTACGAGTGAGACAGGACATCCTAG
AAGGTAGCGAGAGTTATGATGATATGCTGGATGATTCACTTCATCGGACT
TAGAAGACTGTCAATCCTGCATGATTAA

>KLVSKEIGLANAHLAVAPTGSISYLSSCTPSLQPVVSPVEVRKEGALGRV
YVAAWKIDADNYVYYKGA YEVGSEAIINIAAAQKHIDQAISLTLFMTDQAT
TRDLNKAYIQAFKQKCASIYYVRVRQDILEGSESYYDDMLDDFTSSDLEDCQSC
MI*

Sequence description:

FIG. 1 CONT'D

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A] Length 486 bp - 162 aa (Partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-87 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-87 gene sequence. N-terminus to be determined.

ID-196

Clone RS-59(ID-90b)

GTGAGGACATATATTACAAACTTGAATGGACATTCAATCACTAGTACAGC
 ACAAATAGCTCAAAACATGGTAACAGATATAGCAGTAAGCTTAGGTTTTTC
 GTGAGCTGGGAATACATTCTTATCCGATTGATACTGATTCTCCTGAGGAAA
 TGAGTAAGCGTTTAGATGGAATCTGTTCCGGACTTAGAAAAAATGATATTG
 TCATATTTGAGACACCTACATGGAACACTACAACCTTTTGATGAAAAATTAT
 TTCACAAATTAATAATTTTGGTGTAAGATTGTTATTTTATACATGATGT
 TGTACCGCTAATGTTTGATGGAAATTTTATTTGATGGATAGAACTATAGC
 TTATTATAATGAAGCAGATGTTTAATAGCCCCTAGTCAAGCAATGGTCGAT
 AAGCTT

MRTYITNLNGHSITSTAQIAQNMVTDIAVSLGFRELGIHSYPIDTDSPEEMSKRL
 DGICSGLRKNDIVIFQPTWNTTTFDEKLFHKLKIFGVKIVIFIHDVVPLMFDGN
 FYLMDRITAIYYNEADVLIAPSQAMVDKL

Sequence description:

A] Length: 414 bp - 138 aa(partial gene)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence. No obvious signal peptide, but a possible Shine Dalgarno sequence is present upstream of ATG start codon. C-terminus has yet to be determined.

ID-197

Clone RS-59c (ID-90c)

FIG. 1 CONT'D

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CATGGAAATGAAGTTGATGATGTTATTAGAAGGGCATTGGAATATAATCAC
CTTATCTTTGCTTTTGATAATACCTGTCATAACAGAGAGTTAGTATTAGATA
GCAATATCATTTCTCACACAACCTGTGAACAATTGATAAATTTAATGAAAA
ATTTATCAGGCTCCATTATGTATTTGCTAGAGCAACAAAGAGAACAAACA
AGTAATGAAACAAAAGAGCGTTATAAAGAAATATTAGGAGGGTATGGAA
ATGCCTAA

HGNEVDDVIRRAFEYNHLIFAFDNTCHNRELVLDSNIISHTTCEQLINLMKNLS
GSIMYLLEQQREQTSNETKERYKEILGGYGNA*

Sequence description:

A] Length: 261 bp - 87 aa(partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence. N-terminus has yet to be determined

ID-198

Clone RS-70b (ID-93b)

ACATTTTTATATTATGTATTTGAAGACGTAGCCACCCAGTCAAATATGACT
GGGAAGATTTTATAGTATGTCTAAAGAAGAGTTGTCATTTTACCCGTTATT
AAACTTTTAAAGAATCAAGGTGTATACAACGGCTTGATTGGTCTATTCCTC
CTTTATGGGTATATATTTACAGAATCAAGAAATTGTAGCTATTTTTTTAA
TCAATGTGTTGCTAGTTGCTGTTTATGGTGCTTTGACAGTTGATAAAAAAA
TCTTATTAACAGGGTGGTTTACCTATATTAGCTCTTTTAACATTCTTATT
TTAA

TFLYYVFEDVATQSNMTGKIFSMSKEELSYLPVIKLFKNQGVYNGLIGLFLLY
GLYISQNQEIVAIFLINVLLVAVYGALTVDKKILLKQGGLPILALLTFLF*

Sequence description:

A] Length: 312 bp - 104 aa (partial gene sequence)

FIG. 1 CONT'D

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B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence.

N-terminus has yet to be determined

ID-199

Clone RS-70c (ID-93c)

ATGAAATTAAGTGTCCTTGATTATGGGCTTATTGATTATGGAAAACTGCA
AGTGATGCAATACAAGAAACGATTCTTTTATCACAAGAGGCGGAGCAACT
AGGCTATCATCAATTTTGGGTGGCTGAACATCACGGTGTTAAGGCATTTCAG
TATTAGCAATCCAGAATTAATGATAATGCATTTGGCTAACCAGACTAAATC
TATCAAAATTGGCTCTGGAGGTATAATGCCTCTGCACTATAGTAGTTTTAA
ACTCGCGGAGACTCTCAAGACATTAGAGACATGTCATCCGAATCGAGTAA
GTATTGGTTTAGGAAATTCAGTGGGACAGTTAAAGTTTCAAATGCACTTC
GTAGCTTACATAAAGCACATGATTACGAAGAGGTACTGGAGGAATTGAAG
TCATGGCTTATTGATGAATCATCCAGTAAGGAACCATTAGTTCAACCGACT
CTTTCTAGCTTCCCAGACTTATATGTGTTGGGGAGTGGTCAAAAATCAGCT
TATTTAGCGGCTAAACTTGGCTTAGGCTTTACCTTCGGTGTTTTTCCTTTTA
TGGACAAAGACCCATTGACAGAAGCTAAA

MKLSVLDYGLIDYGKTASDAIQETILLSQEAEQLGYHQFWVAEHHGVKAFSIS
NPELMIMHLANQTKSIKIGSGGIMPLHYSSFKLAETLKTLETCHPNRVSIGLGN
SLGTVKVSNALRSLHKAHDYEEVLEELKSWLIDESSSKEPLVQPTLSSFPDLVY
LGSGQKSAYLAAKLGLGFTFGVFPMDKDPLTEAK

Sequence description:

A] Length: 588 bp - 196 aa (partial)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence. No obvious signal peptide, but Shine Dalgarno sequence upstream of the ATG start codon.

FIG. 1 CONT'D

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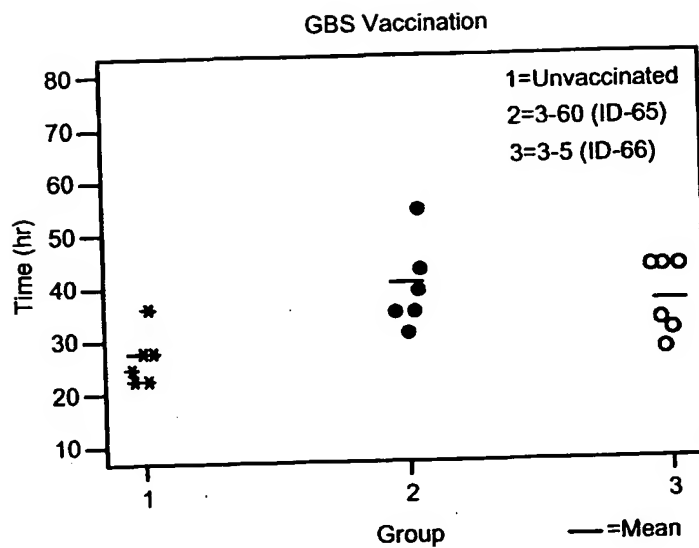


FIG. 2

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nucS1

Bgl II Eco RV

5'-cgagatctgatatctcacaaacagataacggcgtaaataag -3'

nucS2

Bgl II Sma I

5'-gaagatcttccccgggatcacaaacagataacggcgtaaataag -3'

nucS3

Bgl II Eco RV

5'-cgagatctgatatccatcacaaacagataacggcgtaaataag -3'

nucR

Bam HI

5'-cgggatccttatggacctgaatcagcggtgtgc -3'

NucSeq

5'-ggatgctttgtttcaggtgtatc -3'

pTREP_F5'-catgatatcggtacctcaagctcatatcattgtccggcaatgggtgtgggcttttttgttttagcggataa
caatttcacac -3'pTREP_R5'-gcggatcccccggttaattaatgtttaaacactagtcgaagatctcgcgaattctcctgtgtgaaatt
gttatccgcta -3'pUC_F

5'-cgccagggttttcccagtcacgac -3'

V_R

5'-tcaggggggcgagcctatg -3'

V₁

5'-tcgtatgttggtggaattgtg -3'

V₂

5'-tccggctcgtatgttggtggaattg -3'

FIG. 3

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pTREP-Nuc vectors allow cloning of genomic DNA into each frame with respect to the nuclease gene

(i)

pTREP1-nuc1 (EcoRV)	AAGTATCAGATCT-- <u>GATATC</u> --TCACAAACAGATAACGGCGTAAAT	Frame=+1
▲.....	
pTREP1-nuc2 (Sma I)	AAGTATCAGATCTT <u>CCCCGGA</u> --TCACAAACAGATAACGGCGTAAAT	Frame=+2
▲.....	
pTREP1-nuc3 (EcoRV)	AAGTATCAGATCT-- <u>GATATCC</u> ATCACAACAGATAACGGCGTAAAT	Frame=+3
▲.....	
Nuclease Gene	TCACAAACAGATAACGGCGTAAAT	

Cloning site is indicated by an arrow

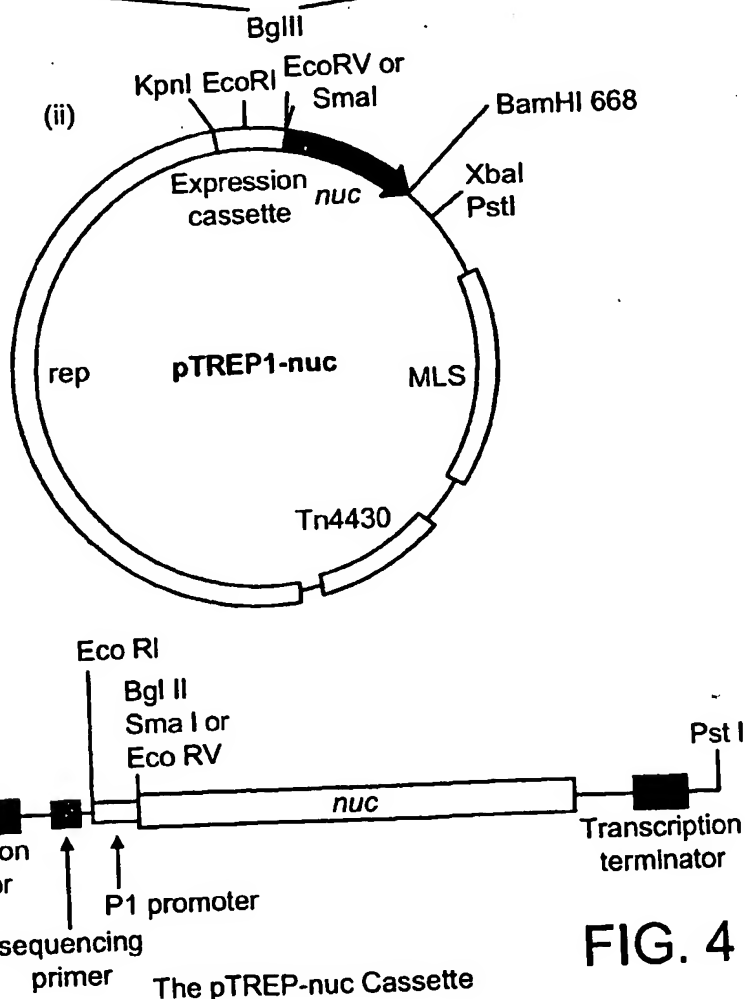
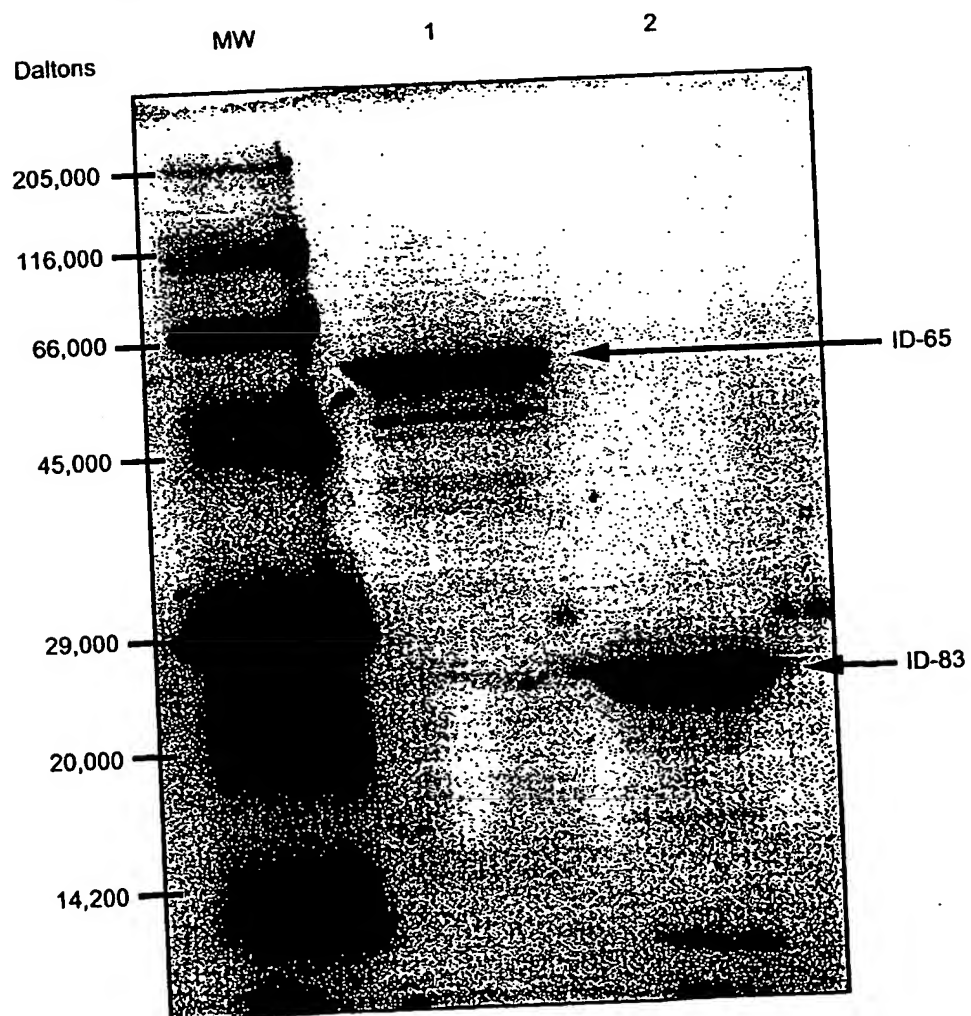


FIG. 4

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FIG. 5

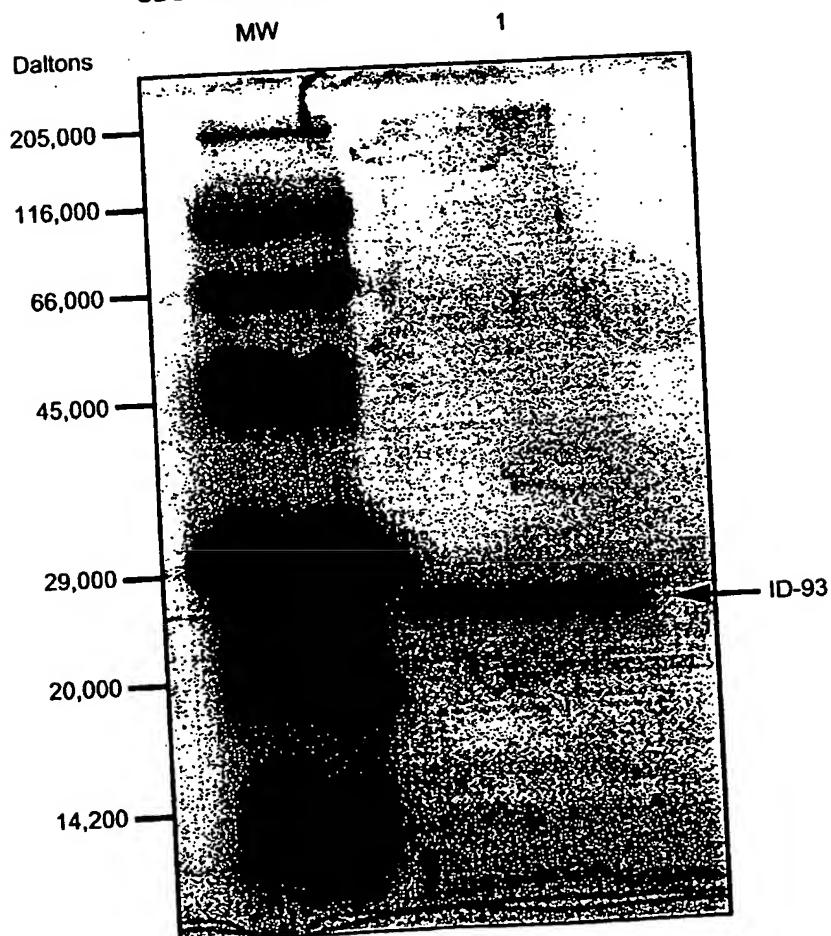
SDS-PAGE analysis of the purified ID-65 and ID-83 protein antigens



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FIG. 6

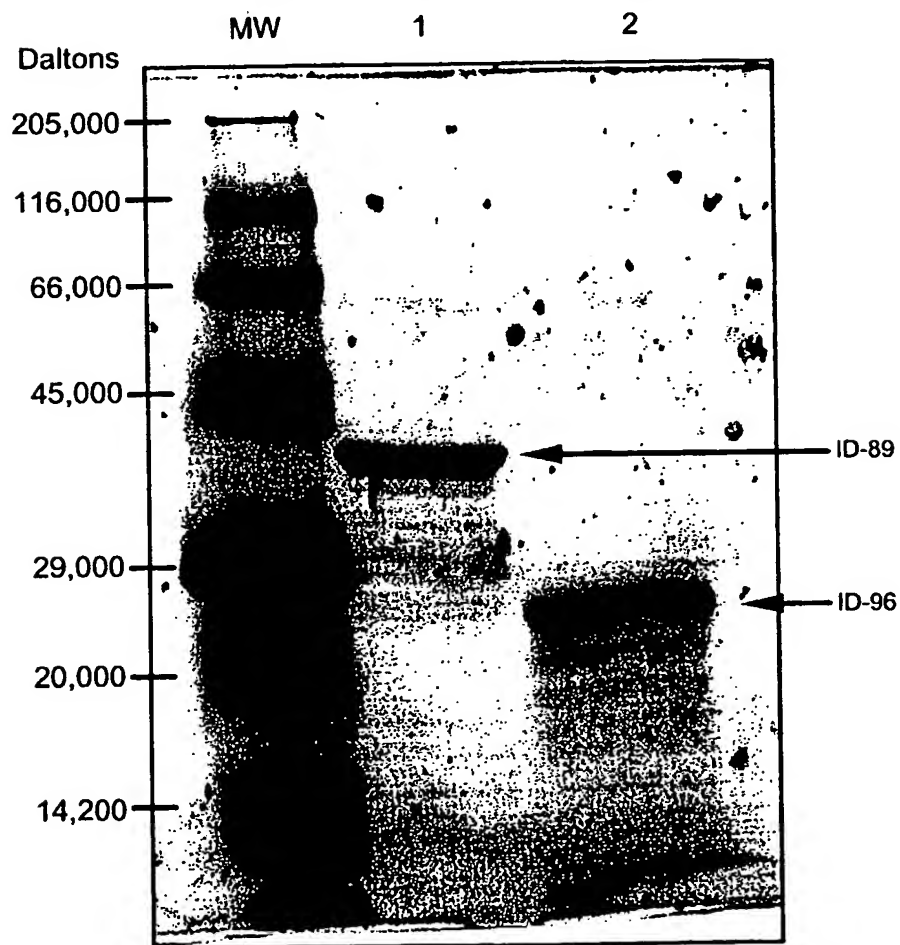
SDS-PAGE analysis of the purified ID-93 antigen



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FIG. 7

SDS-PAGE analysis of the purified ID-89 and ID-96 protein antigens

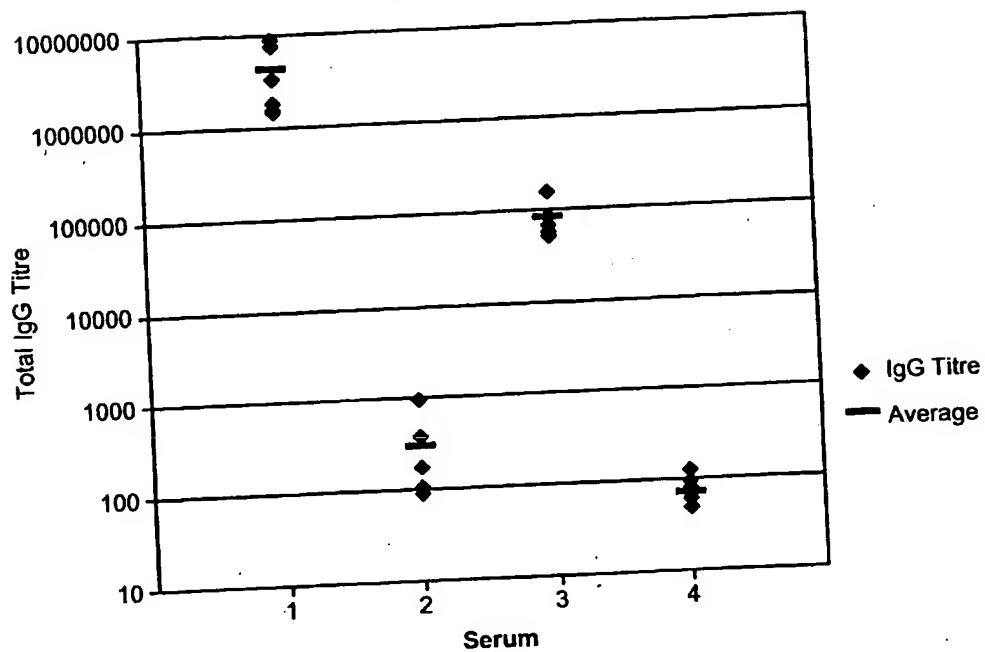


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FIG. 8

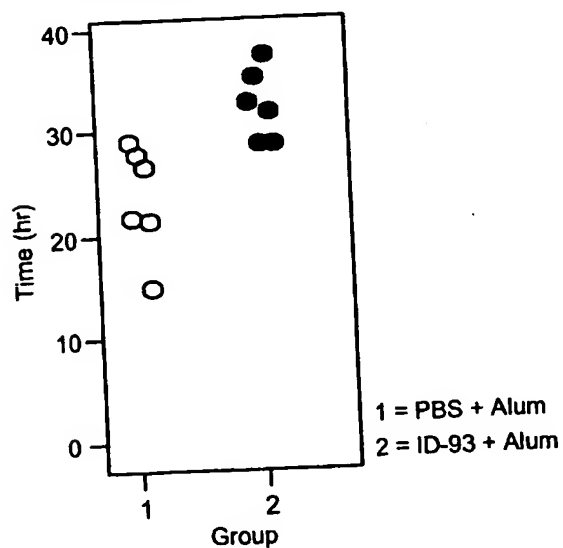
IgG Titres against the ID-65 and ID-83 proteins

ID-65 and ID-83 Vaccinations - IgG Titres

**FIG. 9**

Survival data

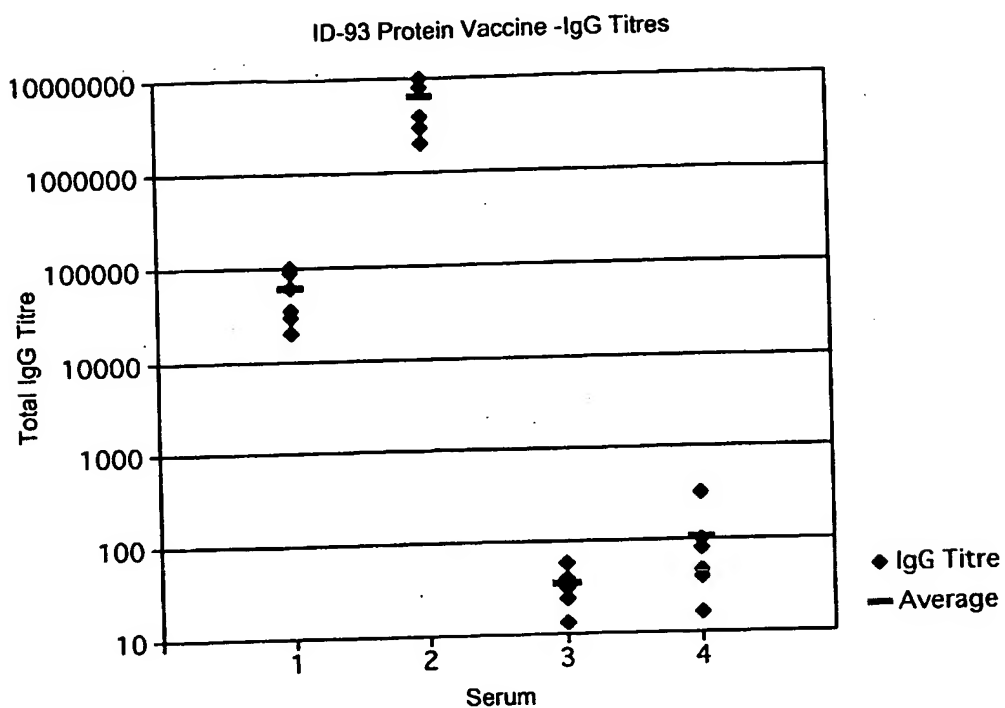
ID-93 Vaccination- GBS Challenge and Survival



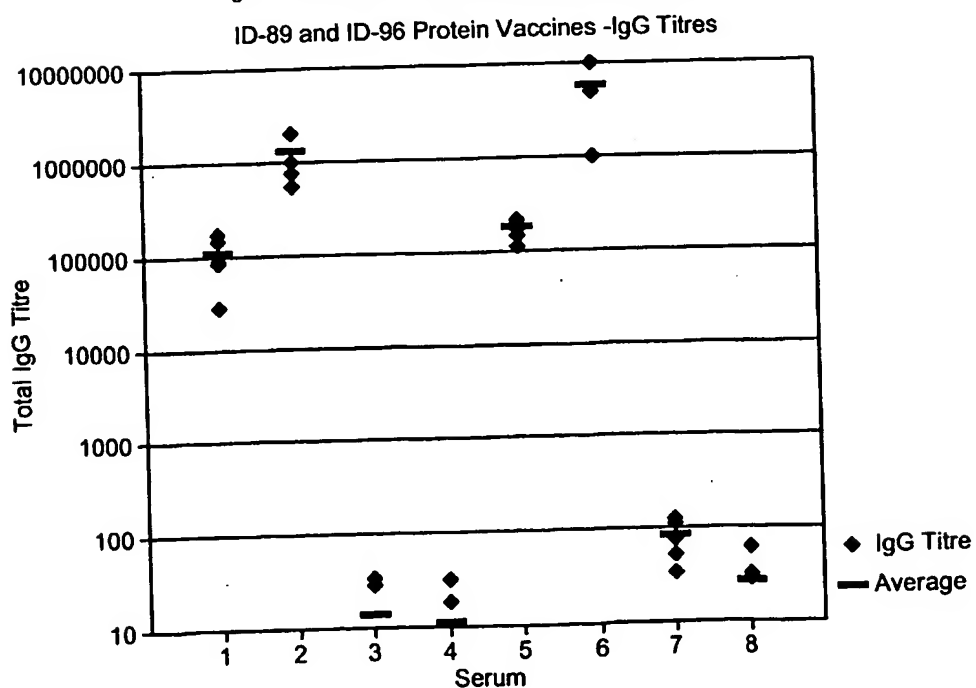
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FIG. 10

IgG Titres against the ID-93 protein

**FIG. 11**

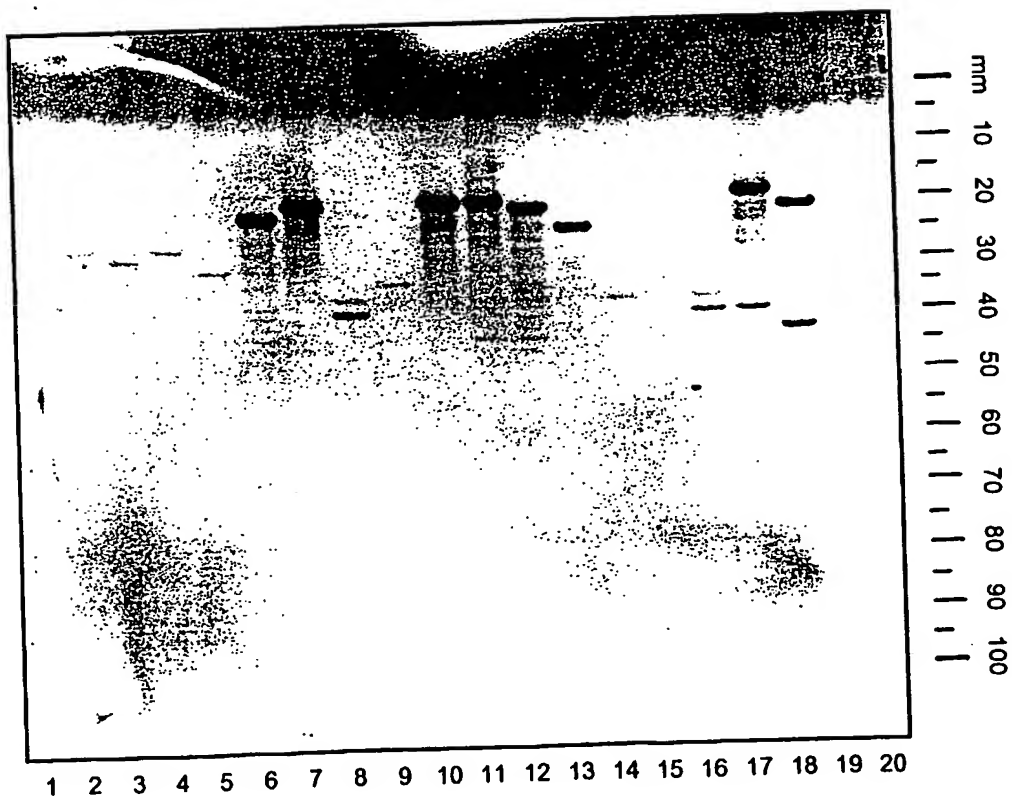
IgG Titres against the ID-89 and ID-96 proteins



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FIG. 12

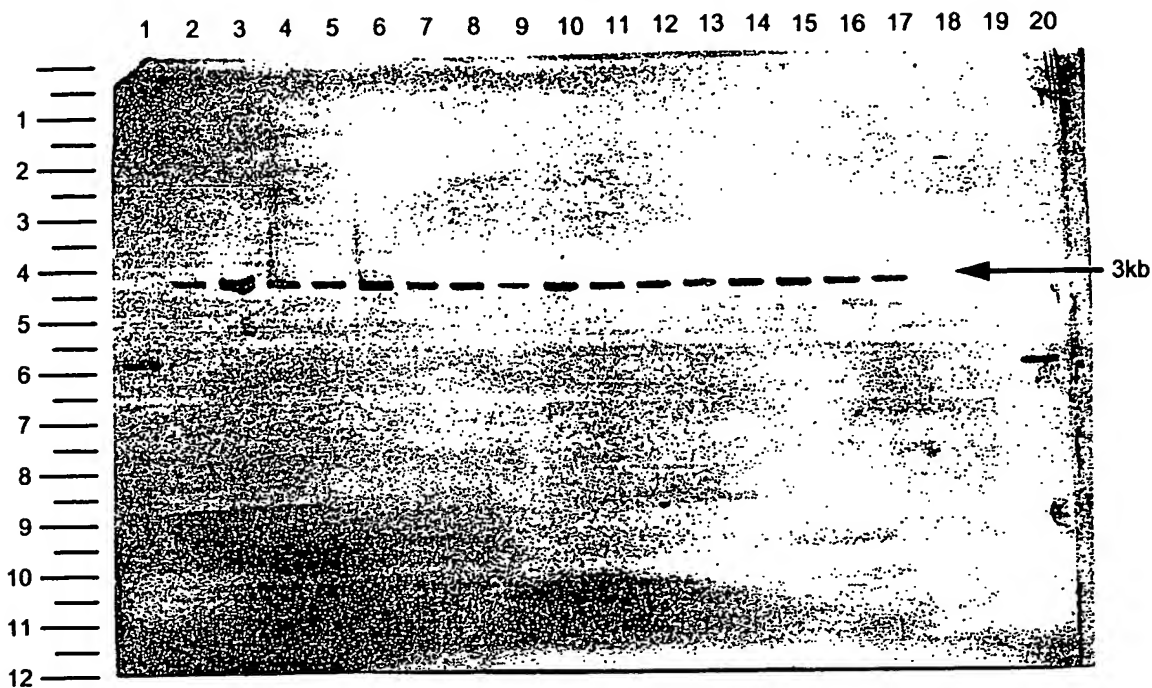
Southern blot analysis - *rib*



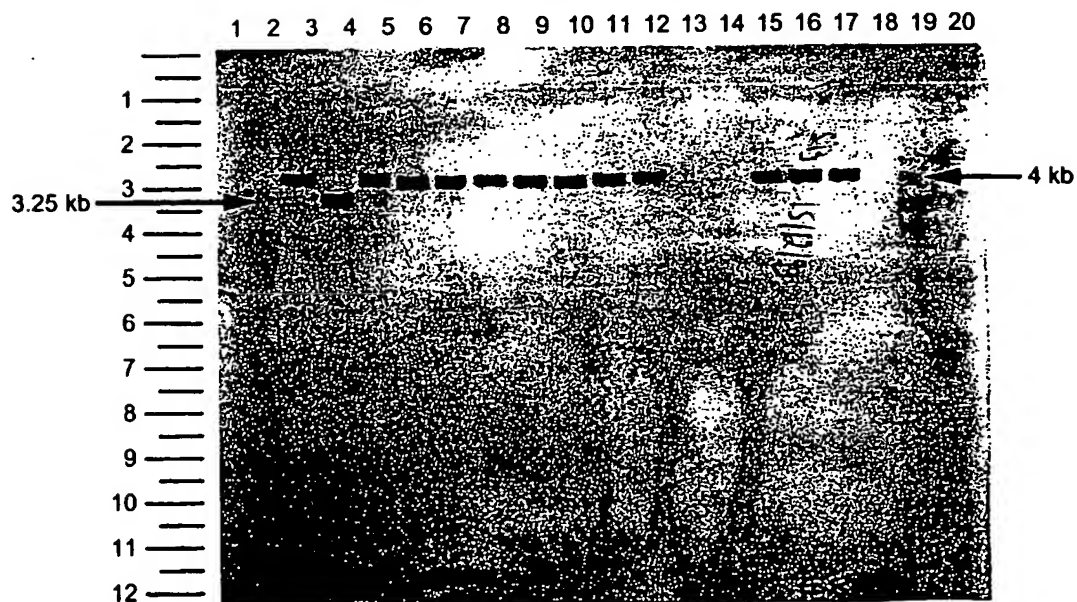
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FIG. 13

Southern blot analysis - ID-65

**FIG. 14**

Southern blot analysis - ID-89

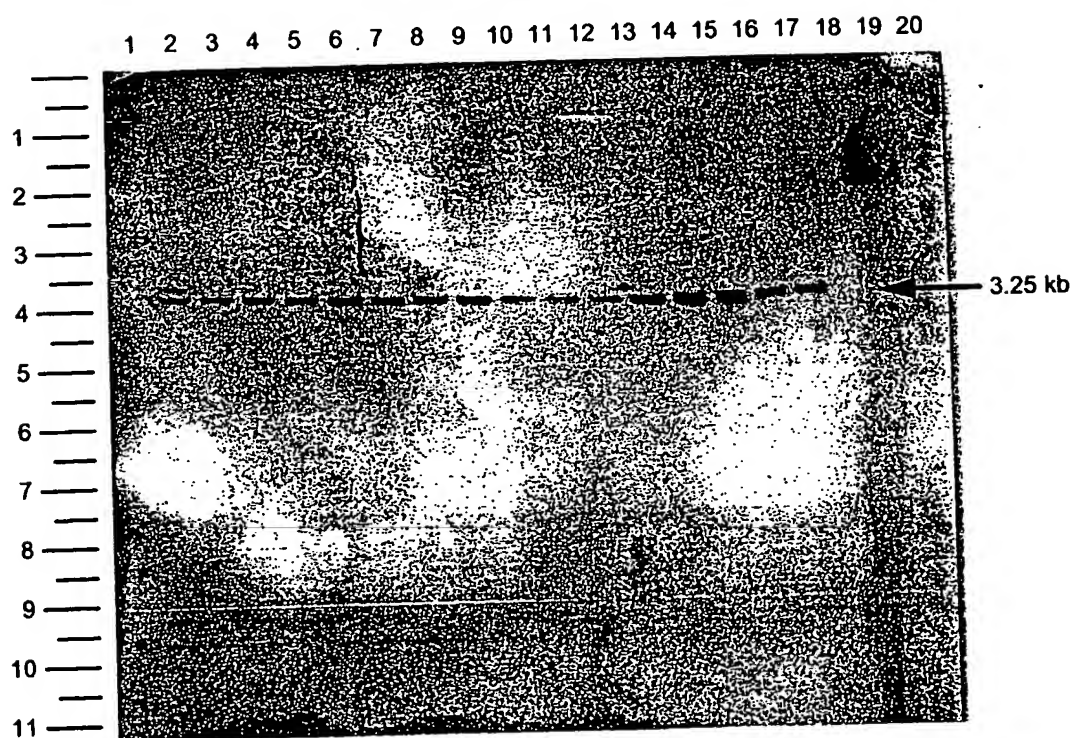


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FIG. 15

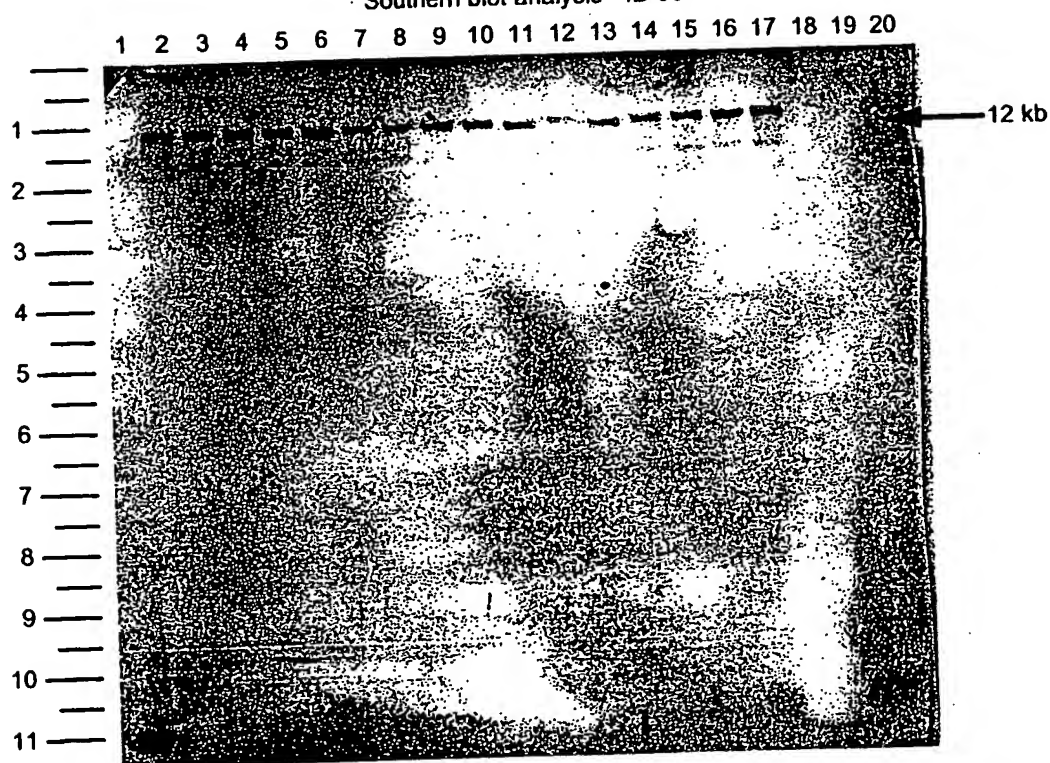
Southern blot analysis - ID-93



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FIG. 16

Southern blot analysis - ID-96



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